

FIG. 1

1 AlaSerCysLeuAsnCysSerAlaSerIleIleProAspArgGluValLeuTyrArgGlu  
GGCCTCCTGCTTGAAGTCTCGGCGAGCATCATACCTGACAGGGAAGTCTCTACCGAGA  
CCGGAGGACGAACTTGACGAGCCGCTCGTAGTATGGACTGTCCCTTCAGGAGATGGCTCT

61 PheAspGluMetGluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeu  
GTTTCGATGAGATGGAAGAGTCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCT  
CAAGCTACTCTACCTTCTCAGAGAGTCTGTAATGGCATGTAGCTCGTTCCCTACTACGA

121 AlaGluGlnPheLysGlnLysAlaLeuGlyLeu  
CGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCC  
CGGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAGG

FIG. 3

1 GlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIleProAsp  
CTGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTGTCCGGGAAGCCGGCAATCATACCTG  
GACCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTATGGAC

61 ArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeuProTyr  
ACAGGGAAGTCTCTACCGAGAGTTCGATGAGATGGAAGAGTGTCTCTCAGCACTTACCGT  
TGTCCCTTCAGGAGATGGCTCTCAAGTACTCTACCTTCTCAGAGAGTCTGTAATGGCA

121 IleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeuLeuGln  
ACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCCTGC  
TGTAAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAGGACG

181 ThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGlnLysLeu  
AGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCTGTCTGCCAGACCAACTGGCAAAAAC  
TCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTTTTTG

241 GluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeuAlaGly  
TCGAGACCTTCTGGGCGAAGCATATGTGGAACCTTCATCAGTGGGATACAATACTTGGCGG  
AGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCATGTTATGAACCGCC

301 LeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAlaAlaVal  
GCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCTGCTG  
CGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAACACCGAAAATGTCGACGAC

361 ThrSerProLeuThrThrSerGln  
TCACCAGCCCACTAACCCTAGCCAAA  
AGTGGTCCGGTGATTGGTGATCGGTTT

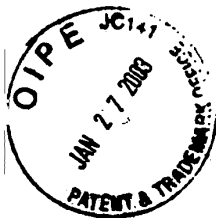
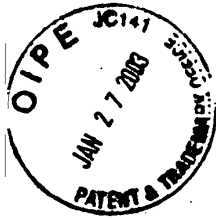


FIG. 2

5-1-1 1 [ggcctcctgcttgaaactgctcggcgagc]ATCATACCTGACAGGGGAAG  
81 1 GTCCGGGAAGCCGGCAATCATACCTGACAGGGGAAG  
91 1 ctggctgctggtcatagtgggcagggctgcttctgtccgggaagccggcaatcatatcctgacaggggaag  
1-2 1 ggtcatagtgggcagggctgcttctgtccgggaagccggcaatcatatcctgacaggggaag  
5-1-1 48 TCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGC  
81 36 TCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGC  
91 70 TCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGC  
1-2 60 TCCTCTATCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGC  
5-1-1 120 TCGCCGAGCAGTTCAAGCAGAAAGGCCCTCGGCCCTCC  
81 108 TCGCCGAGCAGTTCAAGCAGAAAGGCCCTCGGCCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCC  
91 142 TCGCCGAGCAGTTCAAGCAGAAAGGCCCTCGGCCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCC  
1-2 132 TCGCCGAGCAGTTCAAGCAGAAAGGCCCTCGGCC  
81 180 CTGCTGTCCAGACCAACTGGCAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACCTTCATCAGTGGGA  
91 214 CTGCTGTCCAGACCAACTGGCAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACCTTCATCAGTGGGA  
81 252 TACAATACTTGGCGGGCTTGTCAACGCTGCCTGGtaaccccgccattgcttattgatggccttttacagctg  
91 286 TACAATACTTGGCGGGCTTGTCAACGCTGCCTGG  
81 324 ctgtcaccagcccactaaccactagccaaa



## FIG. 4

SerGlyLysProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMet  
1 GTCCGGGAAGCCGCAATCATACCTGACAGGGAAGTCCCTCTACCGAGAGTTCGATGAGAT  
CAGGCCCTTCGGCCGTTAGTAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTA

GluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPhe  
61 GGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGATGATGCTCGCCGAGCAGTT  
CCTTCTCAGGAGTCGTGAATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAA

LysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaPro  
121 CAAGCAGAAGCCCTCGGCCCTCTGCAGACCGCTCCCGTCAGGCAGAGTTATCGCCCC  
GTTTCGTCTTCGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGG

AlaValGlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPhe  
181 TGCTGTCCAGACCAACTGGCAAAACTCGAGACCTTCTGGCGGAAGCATATGTGGAACCTT  
ACGACAGGCTCTGGTTGACCGTTTGTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAA

IleSerGlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAla  
241 CATCAGTGGGATACAATACTTGGCGGGCTTGTCAACGCTGCCCTGGTAACCCCGCATTGC  
GTAGTCACCCCTATGTTATGAACCGCCCGAACAGTTGCGACGGACCATTTGGGCGGTAAACG

SerLeuMetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGln  
301 TTCATTGATGGCTTTACAGCTGCTGTCAACGACCCACATAACCACTAGCCAAA  
AAGTAACTACCGAAAAATGTCGACGACAGTGTCTGGGTGATTGGTGATCGGTTT

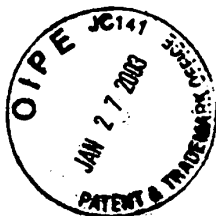


FIG. 5

AspAlaHisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAla  
1 GATGCCCACTTCTATCCAGACAAGCAGAGTGGGAGAACCTTCTTACCTGGTAGCG  
CTACGGGTGAAAGATAGGGTCTGTTTCGTCTCACCCCTCTTGGAAAGGAATGGACCATCGC  
TyrGlnAlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrp  
61 TACCAAGCCACCCTGTGCGCTAGGGCTCAAGCCCTCCCCCATCGTGGGACCATGTGG  
ATGGTTCGGTGGCACACGCGATCCGAGTTCGGGAGGGGTAGCACCTGGTCTACACC  
LysCysLeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeu  
121 AAGTGTTCGCTCAAGCCACCTCCATGGCCAAACACCCCTGCTATACAGACTG  
TTCACAAACTAAGCGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGACGATATGCTCTGAC  
GlyAlaValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCys  
181 GCGGCTGTTTCAGAAATGAATCACCTGACCGACCCAGTCACCAATACATCATGACATGC  
CCGCGACAAGTCTTACTTAGTGGGACTGCGTGGTCAGTGGTTTATGTAGTACTGTACG  
MetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAla  
241 ATGTCGGCCGACCTGGAGTCTGTCACGAGCACCTGGTGTCTGTTGGCGGCTCCTGGCT  
TACAGCCGGCTGGACCTCCAGCAGTCTCGTGGACCCACGAGCAACCGCCGAGGACCCGA  
AlaLeuAlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeu  
301 GCTTTGGCCGCGTATTGCCCTGTCAACAGGCTGCGTGGTCATAGTGGCAGGGTCTCTTG  
CGAAACCGGCGCATAAACGGACAGTGTCCGACGCACCATATCACCCCTCCAGCAGAAC  
-----Overlap with 81-----  
SerGlyLysProAlaIleIleProAspArgGluValLeuTyrArg  
361 TCCGGGAAGCCGGCAATCATACCTGACAGGGAAGTCTCTACCCGAG  
AGGCCCTTCGGCCGTTAGTATGGACTGTCCCTTCAGGAGATGGCTC



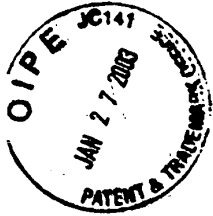


FIG. 6

1 AspAlaHisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAla  
GATGCCCACTTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCG  
CTACGGGTGAAAGATAGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGC

61 TyrGlnAlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrp  
TACCAAGCCACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCATCGTGGGACCAGATGTGG  
ATGGTTCGGTGGCACACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCTGGTCTACACC

121 LysCysLeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeu  
AAGTGTGTTGATTGCGCTCAAGCCCACCTCCATGGGCCAACACCCCTGCTATACAGACTG  
TTCACAACTAAGCGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGAC

181 GlyAlaValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCys  
GGCGCTGTTTCAAGATGAAATCACCTGACGCACCCAGTCACCAAATACATCATGACATGC  
CCGCGACAAGTCTTACTTTAGTGGGACTGCGTGGGTCAAGTGGTTTATGTAGTACTGTACC

241 MetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAla  
ATGTCGGCCGACCTGGAGGTGCTCAGGACACCTGGGTGCTCGTTGGCGGCGTCTGGCT  
TACAGCCGGCTGGACCTCCAGCAGTGTCTGTGACCCACGAGCAACCGCCGAGGACCGA

301 AlaLeuAlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeu  
GCTTTGGCCGCGTATTGCGCTGTCACAGGCTGCGTGGTTCATAGTGGGCAGGGTCTGTTG  
CGAAACCGGCGCATAACGGACAGTTGTCGACGACACAGTATCACCCGTCCAGCAGAAC

361 SerGlyLysProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMet  
TCCCGGAAGCCGGCAATCATACCTGACAGGGAAGTCCTCTACCGAGAGTTTCGATGAGATG  
AGGCCCTTCGGCCGTTAGTATGGACTGTCCCTCAGGAGATGGCTCTCAAGCTACTCTAC

421 GluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPhe  
GAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTC  
CTTCTCACGAGAGTCGTGAATGGCATGTAGCTCGTTCCTACTACGAGCGGCTCGTCAAG

481 LysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaPro  
AAGCAGAAGGCCCTCGGCCTCCTGCAGACCGCTCCGTCAGGCAGAGGTTATCGCCCCCT  
TTCGTCTTCGGGAGCCGGAGGACGTCTGGCGCAGGCAGTCCGTCTCCAATAGCGGGGA

541 AlaValGlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPhe  
GCTGTCCAGACCAACTGGCAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACCTC  
CGACAGGTCTGGTTGACCGTTTTTGTAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAG

601 IleSerGlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAla  
ATCAGTGGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCT  
TAGTCACCTATGTTATGAACCGCCGAACAGTTGCGACGGACCATGGGGCGGTAACGA

661 SerLeuMetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGln  
TCATTGATGGCTTTTACAGCTGCTGTACACAGCCCACTAACCACTAGCCAAA  
AGTAACTACCGAAAATGTGACGACAGTGGTGGGTGATTGGTGATCGGTTT

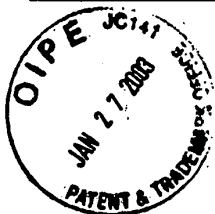


FIG. 7

-----Overlap with 81-----  
PheThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeu  
1 CTTTTACAGCTGCTGTCACCAGCCCACTAACCCTAGCCAAACCCTCCTCTTCAACATAT  
GAAAAATGTCGACGACAGTGGTGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATA  
  
GlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAla  
61 TGGGGGGGTGGGTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCG  
ACCCCCCACCACCGACGGGTGAGCGGGGGGGCCACGGCGATGACGGAACACCCGC  
  
GlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeu  
121 CTGGCTTAGCTGGCGCCGCCATCGGCAGTGTGGACTGGGGAAGGTCTCTCATAGACATCC  
GACCGAATCGACCGCGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGG  
  
AlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGlu  
181 TTGCAGGGTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTG  
AACGTCCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCAC  
  
ValProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeu  
241 AGGTCCCCCTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCC  
TCCAGGGGAGGTGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGG  
  
ValValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAla  
301 TCGTAGTCGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGG  
AGCATCAGCCGCACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCC  
  
ValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSer  
361 CAGTGCAGTGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCC  
GTCACGTCACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGG

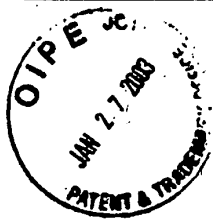


FIG. 8A

SerIleGluThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArg  
1 TCCATTGAGACAATCACGCTCCCCAGGATGCTCTCCCGCACTCAACGTCGGGGCAGG  
AGGTAACCTCTGTAGTCGAGGGGTCTTACGACAGAGGGCGTGAGTTGCAGCCCCCGTCC

ThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGly  
61 ACTGGCAGGGGAAGCCAGGCATCTACAGATTGTGGCACCGGGGAGCGCCCTCCGGC  
TGACCGTCCCCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGGGGGAGGCCG

MetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeu  
121 ATGTTCCGACTCGTCCGTCTCTGTGAGTGCTATGACGAGGCTGTGCTTGTATGAGCTC  
TACAAGCTGAGCAGGACGAGACACTCACGATACTGCGTCCGACACGAACCATCTCGAG

ThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProVal  
181 ACGCCCGCGAGACTACAGTTAGCTACGAGCGTACATGAACACCCCCGGGCTTCCCCGTG  
TGCGGGCGGCTCTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCCGAAGGGCAC

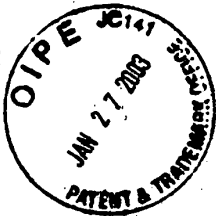


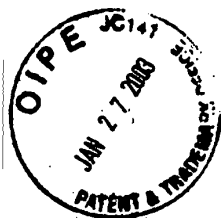
FIG. 8B

-----  
CysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAla  
241 TGCCAGGACCATCTTGAATTTGGAGGGCGTCTTTACAGGCCCTCACTCATATAGATGCC  
ACGGTCCCTGGTAGAACTTAAACCCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGG

-----  
HisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGln  
301 CACTTTCTATCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGCTAGCGTACCAA  
GTGAAAGATAGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTT

-----Overlap with 36-----  
AlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCys  
361 GCCACCGTGTGGCTAGGGCTCAAGCCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGT  
CGGTGGCACACGGGATCCCGAGTTCGGGAGGGGTAGCACCCCTGGTCTACACCTTCACA

-----  
LeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAla  
421 TTGATTGCGCTCAAGCCCAACCCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCT  
AACTAAGCGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCCGCA



## FIG. 9A

1 SerIleGluThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArg  
TCCATTGAGACAATCACGCTCCCCAGGATGCTGTCTCCCGCACTCAACGTCGGGGCAGG  
AGGTAACCTCTGTTAGTGCGAGGGGGTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCC

61 ThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGly  
ACTGGCAGGGGGAAGCCAGGCATCTACAGATTTGTGGCACCAGGGGAGCGCCCTCCGGC  
TGACCGTCCCCCTTCGGTCCGTAGATGTCTAACACCGTGGCCCCCTCGCGGGGAGGCCG

121 MetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeu  
ATGTTCCGACTCGTCCGTCTCTGTGAGTGCTATGACGCAAGGCTGTGCTTGGTATGAGCTC  
TACAAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAG

181 ThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProVal  
ACGCCCCGCCGAGACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTG  
TGCGGGCGGCTCTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCAC

241 CysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAla  
TGCCAGGACCATCTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCC  
ACGGTCTCGGTAGAACTTAAACCCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGG

301 HisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGln  
CACTTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCTTACCTGGTAGCGTACCAA  
GTGAAAGATAGGGTCTGTTTCGTCTACCCCTCTTGGAGGAATGGACCATCGCATGGTT

361 AlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCys  
GCCACCGTGTGCGCTAGGGCTCAAGCCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGT  
CGGTGGCACACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCTGGTCTACACCTTACA

421 LeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTryArgLeuGlyAla  
TTGATTGCGCTCAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCT  
AATAAGCGGAGTTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGA

481 ValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSer  
GTTTCAAGATGAAATCACCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTGCG  
CAAGTCTTACTTTAGTGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACAGC

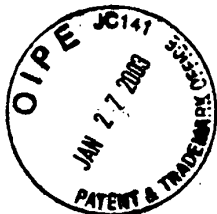
541 AlaAspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeu  
GCCGACCTGGAGGTGCTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCTGGCTGCTTTG  
CGGCTGGACCTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCCGAGGACCGACGAAAC

601 AlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeuSerGly  
GCCGCGTATTGCCTGTCAACAGGCTGCGTGGTCAAGTGGGCAAGGTCGTCTTGTCCGGG  
CGGCGCATAACGGACAGTTGTCCGACGCACCAAGTATCACCCGTCCAGCAGAACAGGCC

661 LysProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGlu  
AAGCCGGCAATCATACCTGACAGGGAAGTCTCTACCGAGAGTTGATGAGATGGAAGAG  
TTCGGCCGTTAGTATGGACTGTCCCTTACGGAGATGGCTCTCAAGCTACTCTACCTTCTC

721 CysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGln  
TGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAG  
ACGAGAGTCGTGAATGGCATGTAGCTCGTTCCTACTACGAGCGGCTCGTCAAGTTCGT

781 LysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaVal  
AAGGCCCTCGGCCCTCTGACAGCCGCTCCCGTCAGGCAGAGGTTATCGCCCTGCTGTC  
TTCCGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAG



## FIG. 9B

841 GlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSer  
CAGACCAACTGGCAAAAACCTCGAGACCTTCTGGGCGAAGCATATGTGGAACCTTCATCAGT  
GTCTGGTTGACCGTTTTTGAAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCA

901 GlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeu  
GGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTG  
CCCTATGTTATGAACGCGCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAAC

961 MetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsn  
ATGGCTTTTACAGCTGCTGTCACCAAGCCCACTAACCCTAGCCAAACCTCCTCTTCAAC  
TACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGACAAGTTG

1021 IleLeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheVal  
ATATTGGGGGGGGTGGGTGGCTGCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTG  
TATAACCCCCCAACCGACGGGTGAGCGGGCGGGGGCCACGGCGATGACGGAAACAC

1081 GlyAlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAsp  
GGCGCTGGCTTAGCTGGCGCCGCCATCGGCAGTGTGGACTGGGGAAGGTCTCATAGAC  
CCGCGACCGAATCGACCGCGGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTG

1141 IleLeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSer  
ATCCTTGCAGGGTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGC  
TAGGAACGTCCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCG

1201 GlyGluValProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGly  
GGTGAGGTCCCCTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGA  
CCACTCCAGGGGAGGTGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCT

1261 AlaLeuValValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGlu  
GCCCTCGTAGTCGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAG  
CGGGAGCATCAGCCGCACCAAGACACGTCGTTATGACGCGGGCGGTGCAACCGGGCCCGCTC

1321 GlyAlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSer  
GGGGCAGTGCAGTGGATGAACGGGCTGATAGCCTTCGCTCCCGGGGGAACCATGTTTCCCC  
CCCCGTCACGTCACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGG

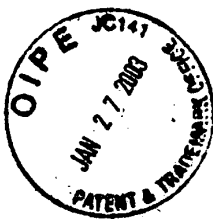


FIG. 10

LeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaValAlaTyrTyrArgGlyLeuAsp  
1 CTCGCCGCAAGCTGGTCGCAATTGGGCATCAATGCCGTGGCCTACTACCGCGTCTTGAC  
GAGCGCGTTTCGACCCAGCGTAACCCGTAGTTACGGCACCGGATGATGGCGCCAGAACTG

ValSerValIleProThrSerGlyAspValValValAlaThrAspAlaLeuMetThr  
61 GTGTCCGTCAATCCGACCAAGCGGCGATGTGTGTCGTGGCAACCGATGCCCTCATGACC  
CACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCACCGTTGGCTACGGGAGTACTGG

GlyTyrThrGlyAspPheAspSerValIleAspTyrAsnThrCysValThrGlnThrVal  
121 GGCTATACCGCGACTTCGACTCGGTGATAGACTACAATACGTGTGTCAACCCAGACAGTC  
CCGATATGGCCGCTGAAGCTGAGCCACTATCTGATGTATGCACACAGTGGTCTGTCTCAG

-----Overlap with  
AspPheSerLeuAspProThrPheThrIleGluThrIleThrLeuProGlnAspAlaVal  
181 GATTTCAGCCTTGACCCCTACCTTCACCAATTGAGACAATCACGCTCCCCCAGGATGCTGTC  
CTAAAGTCGGAACCTGGGATGGAAGTGGTAACCTGTTAGTGCAGAGGGGTCTACGACAG

clone 35-----  
SerArgThrGlnArgArgGlyArgThr  
241 TCCCGCACTCAACGTCGGGGCAGGACTG  
AGGCGGTGAGTTGCAGCCCCCGTCTTGAC

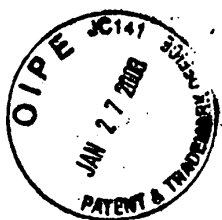


FIG. 11

-----Overlap with 32-----  
1 MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal  
GATGAACCGGCTGATAGCCTTCGCCTCCCGGGGAACCATGTTTCCCCACGCACTACGT  
CTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCA  
61 ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln  
GCCGGAGAGCGATGCAGCTGCCC GCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCA  
CGGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGT  
121 LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer  
GCTCCTGAGGCGACTGCACCAAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTC  
CGAGGACTCCGCTGACGTGGTCACCTATTTCGAGCCTCACATGGTGAGGTACGAGGCCAAG  
181 TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu  
CTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCT  
GACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACCTCGCTGAAATTCTGGACCGA  
241 LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr  
AAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCTTTGTGTCTGCGCAGCGCGGGTA  
TTTTCGATTGAGTACGGTGTCGACGGACCCTAGGGGAAACACAGGACGGTTCGCGCCCAT  
301 LysGlyValTrpArgVal  
TAAGGGGGTCTGGCGAGTG  
ATTCCCCCAGACCGCTCAC



AlaTyrMetSerLysAlaHisGlyIleAspProAsnIleArgThrGlyValArgThrIle  
 1 GGCTTACATGTCCTCAAGGCTCATGGATCGATCCTAACAATCAGGACCGGGTGGAGAACAAAT  
 CCGAATGTACAGGTTCCGAGTACCCCTAGTAGGATTGTAGTCTCTGCCCCACTCTTGTGTA  
 ThrThrGlySerProIleThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCys  
 61 TACCACTGGCAGCCCCATCAGTACTCCACCTACGCAAGTTCCTTCCGACGGCGGTG  
 ATGGTGACCGTCGGGTAGTGATGATGAGGTGGATGCCGTTCAAGAACGGCTGCCGCCAC  
 SerGlyGlyAlaTyrAspIleIleCysAspGluCysHisSerThrAspAlaThrSer  
 121 CTCGGGGGGCGCTTATGACATAATAATTGTGACGAGTGCCACTCCACGGATGCCACATC  
 GAGCCCCCGCGAATACTGTATTATTAAACACTGCTCAGGTGAGGTGCCCTACGGTGTAG  
 IleLeuGlyIleGlyThrValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValVal  
 181 CATCTTGGGCATCGGCACCTGCTCTGACCAAGCAGAGACTGCGGGGCGAGACTGGTGTG  
 GTAGAACCCGTAGCCGTGACAGGAACCTGTTCTCTGACGCCCCCGCTCTGACCAACA  
 LeuAlaThrAlaThrProGlySerValThrValProHisProAsnIleGluValVal  
 241 GCTCGCCACCGCCACCCCTCCGGGCTCCGTCACTGTGCCCCCATCCCAACATCGAGGAGGT  
 CGAGCGGTGGCGGTGGGAGGCCCGAGGCAGTGACACGGGTAGGTTGTAGCTCCTCCA  
 AlaLeuSerThrThrGlyGluIleProPheThrGlyLysAlaIleProLeuGluValIle  
 301 TGCTCTGTCCACCACCGGAGAGATCCCTTTTACGGCAAGGCTATCCCCCTCGAAGTAAT  
 ACGAGACAGGTGGTGGCCTCTCTAGGGAAATAATGCCGTTCCGATAGGGGAGCTTCATTA  
 -----Overlap with 37b-----  
 LysGlyGlyArgHisLeuIlePheCysHisSerLysLysLysCysAspGluLeuAlaAla  
 361 CAAGGGGGGAGACATCTCATCTTCTGTCTCATTTCAAAGAAGAAGTGCAGCAACTCGCCGC  
 GTTCCCCCTCTGTAGAGTAGAAGACAGATAAGTTTCTTCTTTCACGCTGCTTGAGCGGCG  
 LysLeuValAlaLeuGlyIleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerVal  
 421 AAAGCTGGTCGCATGGGCATCAATGCCGTGGCCCTACTACCGCGTCTTGACGTGTCCGT  
 TTTCGACCGGTAAACCGTAGTTACGGCACCGGATGATGGCGCCAGAACTGCACAGGCA  
 -----  
 IleProThr  
 481 CATCCCGACCAG  
 GTAGGGCTGGTC

FIG. 12

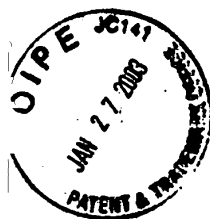


FIG. 13

-----  
1 CysSerLeuThrValThrGlnLeuLeuArgArgLeuHisGlnTrpIleSerSerGluCys  
ACTGCAGCCTCACTGTAACCCAGCTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGT  
TGACGTGGAGTGACATTGGGTCGAGGACTCCGCTGACGTGGTCACCTATTTCGAGCCTCA  
-----  
61 ThrThrProCysSerGlySerTrpLeuArgAspIleTrpAspTrpIleCysGluValLeu  
GTACCACTCCATGCTCCGGTTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGT  
CATGGTGAGGTACGAGGCCAAGGACCGATTCCCTGTAGACCCTGACCTATACGCTCCACA.  
-----  
121 SerAspPheLysThrTrpLeuLysAlaLysLeuMetProGlnLeuProGlyIleProPhe  
TGAGCGACTTTAAGACCTGGCTAAAAGCTAAGCTCATGCCACAGCTGCCCTGGGATCCCCCT  
ACTCGCTGAAATTCTGGACCGATTTTCGATTTCGAGTACGGTGTGACGGACCCTAGGGGA  
-----  
181 ValSerCysGlnArgGlyTyrLysGlyValTrpArgGlyAspGlyIleMetHisThrArg  
TTGTGTCCTGCCAGCGCGGGTATAAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTC  
AACACAGGACGGTCGCGCCCATATTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAG  
-----  
241 CysHisCysGlyAlaGluIleThrGlyHisValLysAsnGlyThrMetArgIleValGly  
GCTGCCACTGTGGAGCTGAGATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCCG  
CGACGGTGACACCTCGACTCTAGTGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGC  
-----  
301 ProArgThrCysArgAsnMetTrpSerGlyThrPheProIleAsnAlaTyrThrThrGly  
GTCCTAGGACCTGCAGGAACATGTGGAGTGGGACCTTCCCCATTAATGCCTACACCACGG  
CAGGATCCTGGACGTCCTGTACACCTCACCTGGAAGGGTAATTACGGATGTGGTGCC  
-----  
361 ProCysThrProLeuProAlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGlu  
GCCCCGTGTACCCCCCTTCCTGCGCCGAACCTACACGTTTCGCGCTATGGAGGGTGTCTGCAG  
CGGGGACATGGGGGAAGGACGCGGCTTGATGTGCAAGCGGATACCTCCCACAGACGTC  
-----  
421 GluTyrValGluIleArgGlnValGlyAspPheHisTyrValThrGlyMetThrThrAsp  
AGGAATATGTGGAGATAAGGCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTG  
TCCTTATACACCTCTATTCCGTCCACCCCTGAAGGTGATGCACTGCCCATACTGATGAC  
-----  
481 AsnLeuLysCysProCysGlnValProSerProGluPhePheThrGlu  
ACAATCTCAAATGCCCCGTGCCAGGTCCCATCGCCGAATTTTTTCACAGAAT  
TGTTAGAGTTTACGGGCACGGTCCAGGGTAGCGGGCTTAAAAAGTGCTTA



## FIG. 14A

AlaTyrMetSerLysAlaHisGlyIleAspProAsnIleArgThrGlyValArgThrIle  
1 TGCTTACATGTCCAAGGCTCATGGGATCGATCCTAACATCAGGACCGGGGTGAGAACAAAT  
ACGAATGTACAGGTTCCGAGTACCCTAGCTAGGATTGTAGTCTGGCCCCACTCTTGTTA

ThrThrGlySerProIleThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCys  
61 TACCACTGGCAGCCCCATCACGTACTCCACCTACGGCAAGTTCTTGCCGACGGCGGGTG  
ATGGTGACCGTCGGGGTAGTGCATGAGGTGGATGCCGTTCAAGGAACGGCTGCCGCCAC

SerGlyGlyAlaTyrAspIleIleIleCysAspGluCysHisSerThrAspAlaThrSer  
121 CTCGGGGGGCGCTTATGACATAATAATTTGTGACGAGTGCCACTCCACGGATGCCACATC  
GAGCCCCCGCAATACTGTATTATTAACACTGCTCACGGTGAGGTGCCACGGTGTAG

IleLeuGlyIleGlyThrValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValVal  
181 CATCTTGGGCATCGGCACTGTCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGT  
GTAGAACCCGTAGCCGTGACAGAACTGGTTCGTCTGACGCCCCCGCTCTGACCAACA

LeuAlaThrAlaThrProProGlySerValThrValProHisProAsnIleGluGluVal  
241 GCTCGCCACC GCCACCCCTCCGGGCTCCGTCACGTGCCCCATCCCAACATCGAGGAGGT  
CGAGCGGTGGCGGTGGGGAGGCCGAGGCAGTGACACGGGGTAGGGTTGTAGCTCCTCCA

AlaLeuSerThrThrGlyGluIleProPheTyrGlyLysAlaIleProLeuGluValIle  
301 TGCTCTGTCCACCACCGGAGAGATCCCTTTTTACGGCAAGGCTATCCCCCTCGAAGTAAT  
ACGAGACAGGTGGTGGCCTCTCTAGGGAAAAATGCCGTTCCGATAGGGGGAGCTTCATTA

LysGlyGlyArgHisLeuIlePheCysHisSerLysLysLysCysAspGluLeuAlaAla  
361 CAAGGGGGGGGAGACATCTCATCTTCTGTCAATCAAAGAAGAAGTGCACGAACTCGCCGC  
GTTCCCCCTCTGTAGAGTAGAAGACAGTAAGTTTCTTCTTACGCTGCTTGAGCGGCG

LysLeuValAlaLeuGlyIleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerVal  
421 AAAGCTGGTCGCATTGGGCATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGTCCGT  
TTTCGACCAGCGTAACCCGTAGTTACGGCACCGGATGATGGCGCCAGAACTGCACAGGCA

IleProThrSerGlyAspValValValValAlaThrAspAlaLeuMetThrGlyTyrThr  
481 CATCCCAGCAGCGCGCATGTTGTCGTGTCGGCAACCGATGCCCTCATGACCGGCTATAC  
GTAGGGCTGGTCGCCCTACAACAGCAGCACCGTTGGCTACGGGAGTACTGGCCGATATG

GlyAspPheAspSerValIleAspTyrAsnThrCysValThrGlnThrValAspPheSer  
541 CGGCGACTTCGACTCGGTGATAGACTACAATACGTGTGTCAACCAGACAGTCGATTTTCAG  
GCCGCTGAAGCTGAGCCACTATCTGATGTTATGCACACAGTGGGTCTGTCACTAAAGTC

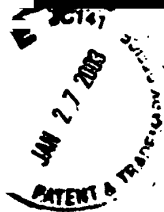
LeuAspProThrPheThrIleGluThrIleThrLeuProGlnAspAlaValSerArgThr  
601 CCTTGACCCTACCTTCACCATGAGACAATCACGCTCCCCAGGATGCTGTCTCCCGCAC  
GGAAGTGGGATGGAAGTGGTAAGTCTGTTAGTGCGAGGGGGTCTACGACAGAGGGCGTG

GlnArgArgGlyArgThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGly  
661 TCAACGTGGGGCAGGACTGGCAGGGGGAAGCCAGGCATCTACAGATTTGTGGCACCAGG  
AGTTGCAGCCCCCTCTGACCGTCCCCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCC

GluArgProSerGlyMetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCys  
721 GGAGCGCCCCCTCCGGCATGTTGACTCGTCCGTCTCTGTGAGTGCTATGACGAGGCTG  
CCTCGCGGGGAGGCCGTACAAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGAC

AlaTrpTyrGluLeuThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThr  
781 TGCTTGGTATGAGCTCAGCCCCGCCGAGACTACAGTTAGGCTACGAGCGTACATGAACAC  
ACGAACCACTCGAGTGCGGGCGGCTCTGATGTCAATCCGATGCTCGCATGTACTTGTG

ProGlyLeuProValCysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeu  
841 CCCGGGGCTTCCCGTGTGCCAGGACCATCTTGAATTTTGGGAGGGCGTCTTTACAGGCCCT  
GGGCCCCGAAGGGCACACGGTCTGGTAGAACTTAAACCTCCCGCAGAAATGTCCGGA



# FIG. 14B

ThrHisIleAspAlaHisPheLeuSerGlnThrLysGlnSerGlyGluAspLeuProTyr  
901 CACTCATATAGATGCCCACTTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTA  
GTGAGTATATCTACGGGTGAAAGATAGGGTCTGTTTCGTCTACCCCTCTTGGAAGGAAT

LeuValAlaTyrGlnAlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAsp  
961 CCTGGTAGCGTACCAAGCCACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCATCGTGGGA  
GGACCATCGCATGGTTCGGTGGCACACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCT

GlnMetTrpLysCysLeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeu  
1021 CCAGATGTGGAAGTGTGTTGATTGCGCTCAAGCCCACCCTCCATGGGCCAACACCCCTGCT  
GGTCTACACCTTCACAACTAAGCGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGA

TyrArgLeuGlyAlaValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIle  
1081 ATACAGACTGGGCGCTGTTTCAAGATGAAATCACCTGACGCACCCAGTCACCAAATACAT  
TATGCTGACCCGCGACAAGTCTTACTTTAGTGGGACTGCGTGGGTCAGTGGTTTATGTA

MetThrCysMetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGly  
1141 CATGACATGCATGTCGGCCGACCTGGAGGTGCTCACGAGCACCTGGGTGCTCGTTGGCGG  
GTACTGTACGTACAGCCGGCTGGACCTCCAGCAGTGTCTGTTGGACCCACGAGCAACCGCC

ValLeuAlaAlaLeuAlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArg  
1201 CGTCCTGGCTGCTTTGGCCGCGTATTGCTGTCAACAGGCTGCGTGGTCATAGTGGGCAG  
GCAGGACCGACGAAACCGGCGCATAACGGACAGTTGTCCGACGCACCAAGTATCACCCGTC

ValValLeuSerGlyLysProAlaIleIleProAspArgGluValLeuTyrArgGluPhe  
1261 GGTGCTCTTGTCGGGAAGCCGGCAATCATACCTGACAGGGAAGTCTCTACCGAGAGTT  
CCAGCAGAACAGGCCCTTCGGCCGTTAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAA

AspGluMetGluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAla  
1321 CGATGAGATGGAAGAGTGTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGC  
GCTACTCTACCTTCTCACGAGAGTCGTGAATGGCATGTAGCTCGTTCCCTACTACGAGCG

GluGlnPheLysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluVal  
1381 CGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCTGACAGACCGCGTCCCGTCAGGCAGAGGT  
GCTCGTCAAGTTCGTCTTCCGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCA

IleAlaProAlaValGlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMet  
1441 TATCGCCCCTGCTGTCCAGACCAACTGGCAAACTCGAGACCTTCTGGGCGAAGCATAT  
ATAGCGGGGACGACAGGTCTGGTTGACCGTTTTTGGACTCTGGAAGACCCGCTTCGTATA

TrpAsnPheIleSerGlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnPro  
1501 GTGGAACCTTCATCAGTGGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCC  
CACCTTGAAGTAGTCACCCTATGTTATGAACCGCCCGAACAGTTGCGACGGACCATTGGG

AlaIleAlaSerLeuMetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGln  
1561 CGCCATTGCTTCATTGATGGCTTTTACAGCTGCTGTACCAAGCCCACTAACCACTAGCCA  
GCGGTAACGAAGTAACCTACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGGT

ThrLeuLeuPheAsnIleLeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAla  
1621 AACCCCTCCTCTTCAACATATTGGGGGGGTGGGTGGCTGCCAGCTCGCCGCCCGGGTGC  
TTGGGAGGAGAAGTTGTATAACCCCCCACCACCGACGGGTCGAGCGGGGGGGGCCACG

AlaThrAlaPheValGlyAlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGly  
1681 CGCTACTGCCTTTGTGGGCGCTGGCTTAGCTGGCGCCGCCATCGGCAGTGTGGACTGGG  
GCGATGACGGAACACCCGCGACCGAATCGACGCGGGG6TAGCCGTCACAACCTGACCC



FIG. 14C

LysValLeuIleAspIleLeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAla  
1741 GAAGGTCCTCATAGACATCCTTGCAAGGTATGGCGCGGGCGTGGCGGGAGCTCTTGTTGGC  
CTTCCAGGAGTATCTGTAGGAACGTCCCATACCGCGCCCGCACCGCCCTCGAGAACACCG

PheLysIleMetSerGlyGluValProSerThrGluAspLeuValAsnLeuLeuProAla  
1801 ATTCAAGATCATGAGCGGTGAGGTCCCCTCCACGGAGGACCTGGTCAATCTACTGCCCGC  
TAAGTTCTAGTACTCGCCACTCCAGGGGAGGTGCCTCCTGGACCAGTTAGATGACGGGCG

IleLeuSerProGlyAlaLeuValValGlyValValCysAlaAlaIleLeuArgArgHis  
1861 CATCCTCTCGCCCGAGCCCTCGTAGTCGGCGTGGTCTGTGCAGCAATACTGCCCGGCA  
GTAGGAGAGCGGGCCTCGGGAGCATCAGCCGCACCAGACACGTCGTTATGACGCGGGCGT

ValGlyProGlyGluGlyAlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArg  
1921 CGTTGGCCCCGGCGAGGGGGCAGTGCAAGTGAACCGGCTGATAGCCTTCGCCCTCCCG  
GCAACCGGGCCCGCTCCCCCGTCACGTACCTACTTGCCGACTATCGGAAGCGGAGGGC

GlyAsnHisValSerProThrHisTyrValProGluSerAspAlaAlaAlaArgValThr  
1981 GGGGAACCATGTTTCCCCCAGCACTACGTGCCGGAGAGCGATGCAGCTGCCCGCGTCAC  
CCCCTTGGTACAAAGGGGGTGCGTGATGCACGGCCTCTCGCTACGTCGACGGGCGCAGTG

AlaIleLeuSerSerLeuThrValThrGlnLeuLeuArgArgLeuHisGlnTrpIleSer  
2041 TGCCATACTCAGCAGCCTCACTGTAACCCAGCTCCTGAGGCGACTGCACCAGTGGATAAG  
ACGGTATGAGTCGTCGGAGTGACATTGGGTGAGGACTCCGCTGACGTGGTCACCTATTC

SerGluCysThrThrProCysSerGlySerTrpLeuArgAspIleTrpAspTrpIleCys  
2101 CTCGGAGTGTAACCACTCCATGCTCCGGTTCCTGGCTAAGGGACATCTGGGACTGGATATG \*  
GAGCCTCACATGGTGAGGTACGAGGCCAAGGACCGATTCCCTGTAGACCCTGACCTATAC

GluValLeuSerAspPheLysThrTrpLeuLysAlaLysLeuMetProGlnLeuProGly  
2161 CGAGGTGTTGAGCGACTTTAAGACCTGGCTAAAAGCTAAGCTCATGCCACAGCTGCCCTGG  
GCTCCACAACCTCGCTGAAATTCTGGACCGATTTTCGATTGAGTACGGTGTGACGGGACC

IleProPheValSerCysGlnArgGlyTyrLysGlyValTrpArgValAspGlyIleMet  
2221 GATCCCTTTGTGTCTGCCAGCGCGGGTATAAGGGGGTCTGGCGAGTGGACGGCATCAT  
CTAGGGGAAACACAGGACGGTCGCGCCCATATTCGCCAGACCGCTCACCTGCCGTAGTA

HisThrArgCysHisCysGlyAlaGluIleThrGlyHisValLysAsnGlyThrMetArg  
2281 GCACACTCGCTGCCACTGTGGAGCTGAGATCACTGGACATGTCAAAAACGGGACGATGAG  
CGTGTGAGCGACGGTGACACCTCGACTCTAGTGACCTGTACAGTTTTTGCCCTGCTACTC

IleValGlyProArgThrCysArgAsnMetTrpSerGlyThrPheProIleAsnAlaTyr  
2341 GATCGTCGGTCCTAGGACCTGCAGGAACATGTGGAGTGGGACCTTCCCCATTAATGCCTA  
CTAGCAGCCAGGATCCTGGACGTCTTGTACACCTCACCTGGAAGGGGTAATTACGGAT

ThrThrGlyProCysThrProLeuProAlaProAsnTyrThrPheAlaLeuTrpArgVal  
2401 CACCACGGGCCCCTGTACCCCCCTTCTGCCGCCGAACACACGTTCCGCGCTATGGAGGGT  
GTGGTGCCCCGGGGACATGGGGGGAAGGACGCGGCTTGATGTGCAAGCGGATACCTCCCA

SerAlaGluGluTyrValGluIleArgGlnValGlyAspPheHisTyrValThrGlyMet  
2461 GTCTGCAGAGGAATATGTGGAGATAAGGCAGGTGGGGGACTTCCACTACGTGACGGGTAT  
CAGACGTCTCCTTATACACCTCTATTCCGTCCACCCCTGAAGGTGATGCACTGCCATA

ThrThrAspAsnLeuLysCysProCysGlnValProSerProGluPhePheThrGlu  
2521 GACTACTGACAATCTCAAATGCCCGTGCCAGGTCCCATGCCCGAATTTTTACAGAAT  
CTGATGACTGTTAGAGTTTACGGGCACGGTCCAGGGTAGCGGGCTAAAAAGTGTCTTA



FIG. 15

AlaValAspPheIleProValGluAsnLeuGluThrThrMetArgSerProValPheThr  
1 GGC GGT G G A C T T T A T C C C T G T G G A G A A C C T A G A G A C A A C C A T G A G G T C C C G G T G T T C A C  
C C G C C A C C T G A A A T A G G G A C A C C T C T T G G A T C T C T G T T G G T A C C A G G G G C C A C A A G T G

AspAsnSerSerProProValValProGlnSerPheGlnValAlaHisLeuHisAlaPro  
61 G G A T A A C T C C T C T C C A C C A G T A G T G C C C C A G A G C T T C C A G G T G G C T C A C C T C C A T G C T C C  
C C T A T T G A G G A G A G G T G G T C A T C A C G G G G T C T C G A A G G T C C A C C A G T G G A G G T A C G A G G

ThrGlySerGlyLysSerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLysVal  
121 C A C A G G C A G C G G C A A A G C A C C A A G G T C C C G G C T G C A T A T G C A G C T C A G G G C T A T A A G G T  
G T G T C C G T C G C C G T T T T C G T G G T T C A G G G C C G A C G T A T A C G T C G A G T C C C G A T A T T C C A

LeuValLeuAsnProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAla  
181 G C T A G T A C T C A A C C C C T C T G T T G C T G C A A C A C T G G G C T T T G G T G C T T A C A T G T C C A A G G C  
C G A T C A T G A G T T G G G G A G A C A A C G A C G T T G T G A C C C G A A A C C A C G A A T G T A C A G G T T C C G

-----Overlap with 40b-----  
HisGlyIleAspProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIle  
241 T C A T G G G A T C G A T C C T A A C A T C A G G A C C G G G G T G A G A A C A A T T A C C A C T G G C A G C C C C A T  
A G T A C C C T A G C T A G G A T T G T A G T C C T G G C C C A C T C T T G T T A A T G G T G A C C G T C G G G G T A

ThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAsp  
301 C A C G T A C T C C A C C T A C G G C A A G T T C C T T G C C G A C G G C G G G T G C T C G G G G G G C G C T T A T G A  
G T G C A T G A G G T G G A T G C C G T T C A A G G A A C G G C T G C C G C C A C G A G C C C C C G C G A A T A C T

IleIleIleCysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThr  
361 C A T A A T A A T T T G T G A C G A G T G C C A C T C C A C G G A T G C C A C A T C C A T C T T G G G C A T T G G C A C  
G T A T T A T T A A A C A C T G C T C A C G G T G A G G T G C C T A C G G T G T A G G T A G A A C C C G T A A C C G T G

ValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrPro  
421 T G T C C T T G A C C A A G C A G A G A C T G C G G G G G C G A G A C T G G T T G T G C T C G C C A C C G C C A C C C C  
A C A G G A A C T G G T T C G T C T G A C G C C C C G C T C T G A C C A A C A C G A G C G G T G G C G G T G G G G

ProGlySerValThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGly  
481 T C C G G G C T C C G T C A C T G T G C C C A T C C C A A C A T C G A G G A G G T T G C T C T G T C C A C C A C C G G  
A G G C C C G A G G C A G T G A C A C G G G G T A G G G T T G T A G C T C C T C C A A C G A G A C A G G T G G T G G C C

GluIleProPheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeu  
541 A G A G A T C C C T T T T T A C G G C A A G G C T A T C C C C C T C G A A G T A A T C A A G G G G G G A G A C A T C T  
T C T C T A G G G A A A A T G C C G T T C C G A T A G G G G G A G C T T C A T T A G T T C C C C C C T C T G T A G A

IlePheCysHisSerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGly  
601 C A T C T T C T G T C A T T C A A A G A A G A A G T G C G A C G A A C T C G C C G C A A A G C T G G T C G C A T T G G G  
G T A G A A G A C A G T A A G T T T C T T C T T C A C G C T G C T T G A G C G G C G T T T C G A C C A G C G T A A C C C

IleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAsp  
661 C A T C A A T G C C G T G G C C T A C T A C C G C G G T C T T G A C G T G T C C G T C A T C C C G A C C A G C G G C G A  
G T A G T T A C G G C A C C G G A T G A T G G C G C C A G A A C T G C A C A G G C A G T A G G G C T G G T C G C C G C T

ValValValValAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerVal  
721 T G T T G T C G T C G T G G C A A C C G A T G C C C T A T G A C C G G C T A T A C C G G C G A C T T C G A C T C G G T  
A C A A C A G C A G C A C C G T T G G C T A C G G G A G T A C T G G C C G A T A T G G C C G T G A A G C T G A G C C A

IleAspCysAsnThrCys  
781 G A T A G A C T G C A A T A C G T G T G  
C T A T C T G A C G T T A T G C A C A C



FIG. 16

ProCysThrCysGlySerSerAspLeuTyrLeuValThrArgHisAlaAspValIlePro  
1 CTCCCTGCACTTGCGGCTCCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATTG  
GAGGGACGTGAACGCCGAGGAGCCTGGAAATGGACCACTGCTCCGTGCGGCTACAGTAAG  
ValArgArgArgGlyAspSerArgGlySerLeuLeuSerProArgProIleSerTyrLeu  
61 CCGTGCGCCGGCGGGGTGATAGCAGGGGCGAGCCTGCTGTCGCCCCGGGCCATTTCTACT  
GGCAGCGCGGCCGCCCACTATCGTCCCCGTGCGACGACAGCGGGGCCGGGTAAAGGATGA  
LysGlySerSerGlyGlyProLeuLeuCysProAlaGlyHisAlaValGlyIlePheArg  
121 TGAAGGCTCCTCGGGGGGTCCGCTGTTGTGCCCCGCGGGGACGCCGTGGGCATATTTA  
ACTTTCCGAGGAGCCCCCAGGCGACAACACGGGGCGCCCCGTGCGGCACCCGTATAAAT  
-----Overlap with  
AlaAlaValCysThrArgGlyValAlaLysAlaValAspPheIleProValGluAsnLeu  
181 GGGCCGCGGTGTGCACCCGTGGAGTGGCTAAGGCGGTGGACTTTATCCCTGTGGAGAACC  
CCCGGCCACACGTGGGCACCTCACCGATTCCGCCACCTGAAATAGGGACACCTCTTGG  
33c-----  
GluThrThrMetArgSerProValPheThrAspAsnSer  
241 TAGAGACAACCATGAGGTCCCCGGTGTTACGGATAACTCCTC  
ATCTCTGTTGGTACTCCAGGGGCCACAAGTGCCTATTGAGGAG

FIG. 17

GlyTrpArgLeuLeuAlaProIleThrAlaTyrAlaGlnGlnThrArgGlyLeuLeuGly  
1 GGGGTGGAGGTTGCTGGCGCCCATCACGGCGTACGCCAGCAGACAAGGGGCTCTAGG  
CCCCACCTCCAACGACCGCGGGTAGTGCCGCATGCGGGTCTGTTCCCCGGAGGATCC  
CysIleIleThrSerLeuThrGlyArgAspLysAsnGlnValGluGlyGluValGlnIle  
61 GTGCATAATCACCAGCCTAACTGGCCGGGACAAAAACCAAGTGGAGGGTGAGGTCCAGAT  
CACGTATTAGTGGTCGGATTGACGGCCCTGTTTTTGGTTACCTCCCACTCCAGGTCTA  
ValSerThrAlaAlaGlnThrPheLeuAlaThrCysIleAsnGlyValCysTrpThrVal  
121 TGTGTCAACTGCTGCCCAAACCTTCTGGCAACGTGCATCAATGGGGTGTGCTGGACTGT  
ACACAGTTGACGACGGGTTTGGAAAGGACCGTTGCACGTAGTTACCCACACGACCTGACA  
TyrHisGlyAlaGlyThrArgThrIleAlaSerProLysGlyProValIleGlnMetTyr  
181 CTACCACGGGGCCGGAACGAGGACCATCGCGTCACCCAAGGGTCTGTCTATCCAGATGTA  
GATGGTGCCCCGGCCTTGCTCCTGGTAGCGAGTGGGTTCCAGGACAGTAGGTCTACAT  
ThrAsnValAspGlnAspLeuValGlyTrpProAlaProGlnGlySerArgSerLeuThr  
241 TACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCCGCAAGGTAGCCGCTCATTGAC  
ATGGTTACATCTGGTTCTGGAACACCCGACCGGGCGAGGCGTTCCATCGGCGAGTAAGT  
-----Overlap with 8h-----  
ProCysThrCysGlySerSerAspLeuTyrLeuValThrArgHis  
301 ACCCTGCACTTGCGGCTCCTCGGACCTTTACCTGGTCACGAGGCACG  
TGGGACGTGAACGCCGAGGAGCCTGGAAATGGACCACTGCTCCGTGC



FIG. 18

-----  
1 AsnMetTrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeu  
GAACATGTGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCTGTACCCCCCT  
CTTGACACCTCACCCTGGAAGGGTAATTACGGATGTGGTGGCCGGGGACATGGGGGA  
-----Overlap with 25c-----  
61 ProAlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIle  
TCCTGCGCCGAACCTACACGTTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGAT  
AGGACGCGGGCTTGATGTGCAAGCGCGATACCTCCACAGACGTCTCCTTATGCACCTCTA  
-----  
121 ArgGlnValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysPro  
AAGGCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCC  
TTCCGTCCACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAAATTTACGGG  
-----  
181 CysGlnValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPhe  
GTGCCAGGTCCCATCGCCGAATTTTTACAGAATTGGACGGGGTGGCGCTACATAGGTT  
CACGGTCCAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAA  
-----  
241 AlaProProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGlu  
TGCGCCCCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTAGAGTAGGACTCCACGA  
ACGCGGGGGGACGTTGCGGAACGACGCCCTCTCCATAGTAAGTCTCATCTGAGGTGCT  
-----  
301 TyrProValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSer  
ATACCCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTC  
TATGGGCCATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAG  
-----  
361 MetLeuThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGly  
CATGCTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGG  
GTACGAGTGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCGCTTCCAACCGCTCCCC  
-----  
421 SerProProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAla  
ATACCCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGC  
TAGTGGGGGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCG  
-----  
481 ThrCysThrAlaAsnHisAspSerProAsp  
AACTTGACCGCTAACCATGACTCCCCTGAT  
TTGAACGTGGCGATTGGTACTGAGGGGACTA





FIG. 19

-----Overlap with 14c-----  
1 SerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCysThrAlaAspHis  
AGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGACCCGCTAACCAT  
TCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACGTGGCGATTGGTA  
-----  
61 AspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGlnGluMetGlyGlu  
GACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAGGAGATGGGCGGC  
CTGAGGGGACTACGACTCGAGTATCTCCGTTGGAGGATACCTCCGTCCTTACCCGCCG  
-----  
121 AsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSerPheAspProLeu  
AACATCACCAGGGTTGAGTCAGAAAACAAAGTGTTGATTCTGGACTCCTTCGATCCGCTT  
TTGTAGTGTTCCCAACTCAGTCTTTTGTTCACCACTAAGACCTGAGGAAGCTAGGCGAA  
-----  
181 ValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeuArgLysSerArg  
GTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCCTGCGGAAGTCTCGG  
CACCGCCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGACGCCCTCAGAGCC  
-----  
241 ArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnProProLeuValGlu  
AGATTCGCCCAGGCCCTGCCGTTTGGGCGCGGCCGACTATAACCCCCCGCTAGTGGAG  
TCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCTGATATTGGGGGGCGATCACCTC  
-----  
301 ThrTrpLysLysProAspTyrGluProProValValHisGlyCysProLeuProProPro  
ACGTGGAAAAAGCCCGACTACGAACACCTGTGGTCCATGGCTGTCCGCTTCCACCTCCA  
TGCACCTTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACAGGCGAAGGTGGAGGT  
-----  
361 LysSerProProValPro  
AAGTCCCCTCCTGTGCCG  
TTCAGGGGAGGACACGGC

FIG. 20

-----  
1 ValTrpAlaArgProAspTyrAsnProProLeuValGluThrTrpLysLysProAspTyr  
CGTTTGGGCGCGGCCGACTATAACCCCCCGCTAGTGGAGACGTGGAAAAAACCCGACTA  
GCAAAACCCGCGCCGGCTGATATTGGGGGGCGATCACCTCTGCACCTTTTTTGGGCTGAT  
-----  
-----Overlap with 8f-----  
61 GluProProValValHisGlyCysProLeuProProProLysSerProProValProPro  
CGAACCCACCTGTGGTCCATGGCTGCCGCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCC  
GCTTGGTGGACACCAGGTACCGACGGGCGAAGGTGGAGGTTTCAGGGGAGGACACGGAGG  
-----  
121 ProArgLysLysArgThrValValLeuThrGluSerThrLeuSerThrAlaLeuAlaGlu  
GCCTCGGAAGAAGCGGACGGTGGTCTCACTGAATCAACCCTATCTACTGCCTTGGCCGA  
CGGAGCCTTCTTCGCTGCCACCAGGAGTGACTTAGTTGGGATAGATGACGGAACCGGCT  
-----  
181 LeuAlaThrArgSerPheGlySerSerSerThrSerGlyIleThrGlyAspAsnThrThr  
GCTCGCCACCAGAAGCTTTGGCAGCTCCTCAACTTCCGGCATTACGGGCGACAATACGAC  
CGAGCGGTGGTCTTCGAAACCGTCGAGGAGTTGAAGGCCGTAATGCCCGCTGTTATGCTG  
-----  
241 ThrSerSerGluProAlaProSerGlyCysProProAspSerAspAlaGluSerPhe  
AACATCCTCTGAGCCCGCCCTTCTGGCTGCCCCCGACTCCGACGCTGAGTCTTTGCT  
TTGTAGGAGACTCGGGCGGGGAAGACCGACGGGGGGGCTGAGGCTGCGACTCAGGAAACG

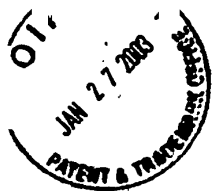


FIG. 21

-----  
1 AlaSerArgSerPheGlySerSerSerThrSerGlyIleThrGlyAspAsnThrThrThr  
GCCTCCAGAAGCTTTGGCAGCTCCTCAACTTCCGGCATTACGGGCGACAATACGACAACA  
CGGAGGTCTTCGAAACCGTCGAGGAGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGT  
-----Overlap with 33f-----  
61 SerSerGluProAlaProSerGlyCysProProAspSerAspAlaGluSerTyrSerSer  
TCCTCTGAGCCCGCCCTTCTGGCTGCCCCCGACTCCGACGCTGAGTCCTATTCTCTCC  
AGGAGACTCGGGCGGGGAAGACCGACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGG  
121 MetProProLeuGluGlyGluProGlyAspProAspLeuSerAspGlySerTrpSerThr  
ATGCCCCCCTGGAGGGGGAGCCTGGGGATCCGGATCTTAGCGACGGGTGATGGTCAACG  
TACGGGGGGGACCTCCCCCTCGGACCCCTAGGCCTAGAATCGCTGCCAGTACCAAGTTGC  
181 ValSerSerGluAlaAsnAlaGluAspValValCysCysSerMetSerTyrSerTrpThr  
GTCAGTAGTGAGGCCAACGCGGAGGATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACA  
CAGTCATCACTCCGGTTGCGCTCTACAGCACACGACGAGTTACAGAATGAGAACCTGT  
241 GlyAlaLeuValThrProCysAlaAlaGluGluGlnLysLeuProIleAsnAlaLeuSer  
GGCGCACTCGTCACCCCGTGCGCCGCGGAAGAACAAGAACTGCCATCAATGCACTAAGC  
CCGCGTGAGCAGTGGGGCACGCGGCGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTGC  
301 AsnSerLeuLeuArgHisHisAsnLeuValTyrSerThrThrSerArgSer  
AACTCGTTGCTACGTCAACCAATTTGGTGTATTCCACCACCTCAGCGAGTG  
TTGAGCAACGATGCAGTGGTGTAAACCACATAAGGTGGTGGAGTGCGTCAC

FIG. 22

1 GlyThrTyrValTyrAsnHisLeuThrProLeuArgAspTrpAlaHisAsnGlyLeuArg  
GGCACCTATGTTTATAACCATCTGACTCCTCTTCGGGACTGGGCGCACAAAGGCTTGCAG  
CCGTGGATACAAATATTGGTAGAGTGAGGAGAAGCCCTGACCCGCGTGTGCGGAACGCT  
61 AspLeuAlaValAlaValGluProValValPheSerGlnMetGluThrLysLeuIleThr  
GATCTGGCCGTGGCTGTAGAGCCAGTCGTCTTCTCCCAATGGAGACCAAGCTCATCACG  
CTAGACCGGCACCGACATCTCGGTCAGCAGAAAGAGGGTTTACCTCTGGTTCGAGTAGTGC  
121 TrpGlyAlaAspThrAlaAlaCysGlyAspIleIleAsnGlyLeuProValSerAlaArg  
TGGGGGGGAGATACCGCCGCGTGGGTGACATCATCAACGGCTTGCTGTTTCCGCCCCG  
ACCCCCGTCTATGGCGGCGCACGCCACTGTAGTAGTTGCCGAACGGACAAAGGCGGGCG  
-----  
181 ArgGlyArgGluIleLeuLeuGlyProAlaAspGlyMetValSerLysGlyTrpArgLeu  
AGGGGCCGGGAGATACTGCTCGGGCCAGCCGATGGAATGGTCTCCAAGGGTTGGAGGTTG  
TCCCCGGCCCTCTATGACGAGCCCGGTGCGCTACCTTACCAGAGGTTCCCAACCTCCAAC  
241 LeuAlaProIleThrAlaTyrAlaGlnGlnThrArgGlyLeuLeuGlyCysIleIleThr  
CTGGCGCCCATCACGGCGTACGCCCAGCAGACAAGGGGGCCTCCTAGGGTGCATAATCACC  
GACCGCGGGTAGTGCCGCATGCGGGTCGTCTGTTCCCGGAGGATCCACGTATTAGTGG  
-----Overlap with 7e-----  
301 SerLeuThrGlyArgAspLysAsnGlnValGluGlyGluValGlnIleValSerThrAla  
AGCCTAACTGGCCGGGACAAAAACCAAGTGGAGGGTGAGGTCCAGATTGTGTCAACTGCT  
TCGGATTGACCGGCCCTGTTTTTGGTTACCTCCCACTCCAGGTCTAACACAGTTGACGA  
-----  
361 AlaGlnThrPheLeuAlaThrCysIleAsnGlyValCysTrp  
GCCCCAACCTTCTGGCAACGTGCATCAATGGGGTGTGCTGG  
CGGGTTTGGAAGGACCGTTGCACGTAGTTACCCACACGACC



## FIG. 23

1 GlyGlyValValLeuValGlyLeuMetAlaLeuThrLeuSerProTyrTyrLysArgTyr  
GGCGGTGTTGTTCTCGTTCGGGTTGATGGCGCTGACTCTGTCACCATATTACAAGCGCTAT  
CCGCCACAACAAGAGCAGCCCACTACCGCGACTGAGACAGTGGTATAATGTTCCGCGATA

61 IleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeuThrArgValGluAlaGlnLeuHis  
ATCAGCTGGTGCTTGTGGTGCTTCAGTATTTTCTGACCAGAGTGAAGCGCAACTGCAC  
TAGTCGACCACGAACACCACCGAAGTCATAAAAGACTGGTCTCACCTTCGCGTTGACGTG

121 ValTrpIleProProLeuAsnValArgGlyGlyArgAspAlaValIleLeuLeuMetCys  
GTGTGGATTCCCCCCTCAACGTCCGAGGGGGGCGCGACGCCGTCTACTCATGTGT  
CACACCTAAGGGGGGAGTTGCAGGCTCCCCCGCGCTGCGGCAGTAGAATGAGTACACA

181 AlaValHisProThrLeuValPheAspIleThrLysLeuLeuLeuAlaValPheGlyPro  
GCTGTACACCCGACTCTGGTATTTGACATCACCAAATTGCTGCTGGCGCTCTTCGGACCC  
CGACATGTGGGTGAGACCATAAACTGTAGTGGTTTAACGACGACCGGCAGAAGCCTGGG

241 LeuTrpIleLeuGlnAlaSerLeuLeuLysValProTyrPheValArgValGlnGlyLeu  
CTTTGGATTCTTCAAGCCAGTTTGCTTAAAGTACCCTACTTTGTGCGCGTCCAAGGCCTT  
GAAACCTAAGAAGTTCCGTCAAACGAATTTTCATGGGATGAAACACGCGCAGGTTCCGGAA

301 LeuArgPheCysAlaLeuAlaArgLysMetIleGlyGlyHisTyrValGlnMetValIle  
CTCCGGTTCTGCGCGTTAGCGCGGAAGATGATCGGAGGCCATTACGTGCAAATGGTCATC  
GAGGCCAAGACGCGCAATCGCGCCTTCTACTAGCCTCCGGTAATGCACGTTTACCAGTAG

-----  
361 IleLysLeuGlyAlaLeuThrGlyThrTyrValTyrAsnHisLeuThrProLeuArgAsp  
ATTAAGTTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCACTCCTCTTCGGGAC  
TAATTCAATCCCCGGAATGACCGTGATACAAATATTGGTAGAGTGAGGAGAAGCCCTG

-----Overlap with 7f -----  
421 TrpAlaHisAsnGlyLeuArgAspLeuAlaValAlaValGluProValValPheSerGln  
TGGGCGCACACGGCTTGCGAGATCTGGCCGTGGCTGTAGAGCCAGTCGTCTTCTCCCAA  
ACCCGCGTGTGCGGAACGCTCTAGACCGGCACCGACATCTCGGTACGAGAAGAGGGTT

-----  
481 MetGluThrLysLeuIleThrTrpGly  
ATGGAGACCAAGCTCATCAGTGGGGGGC  
TACCTCTGGTTCGAGTAGTGCACCCCCCG



FIG. 24

1 GluTyrValValLeuLeuPheLeuLeuLeuAlaAspAlaArgValCysSerCysLeuTrp  
GGGAGTACGTCGTTCTCCTGTTCTTCTGCTTGCAGACGCGCGCTGCTCCTGCTTGT  
CCCTCATGCAGCAAGAGGACAAGGAAGACGAACGTCTGCGCGCGCAGACGAGGACGAACA

61 MetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsnLeuValIleLeuAsnAla  
GGATGATGCTACTCATATCCCAAGCGGAGGCGGCTTTGGAGAACCCTCGTAATACTTAATG  
CCTACTACGATGAGTATAGGGTTCGCCTCCGCCGAAACCTCTTGAGCATTATGAATTAC

121 AlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuValPhePheCysPheAlaTrp  
CAGCATCCCTGGCCGGGACGCACGGTCTTGATCCTTCTCGTGTCTTCTGCTTTGCAT  
GTCTAGGGACCGGCCCTGCGTGCCAGAACATAGGAAGGAGCACAAGAAGACGAAACGTA

181 TyrLeuLysGlyLysTrpValProGlyAlaValTyrThrPheTyrGlyMetTrpProLeu  
GGTATTTGAAGGGTAAGTGGGTGCCCCGAGCGGTCTACACCTTCTACGGGATGTGGCCTC  
CCATAAACTTCCCATTACCCACGGGCCTCGCCAGATGTGGAAGATGCCCTACACGGGAG

241 LeuLeuLeuLeuLeuAlaLeuProGlnArgAlaTyrAlaLeuAspThrGluValAlaAla  
TCCTCCTGCTCCTGTTGGCGTTGCCCCAGCGGGCGTACGCGCTGGACACGGAGGTGGCCG  
AGGAGGACGAGGACAACCGCAACGGGGTTCGCCGCATGCGCGACCTGTGCCTCCACGGG

-----Overlap with 11b-----

301 SerCysGlyGlyValValLeuValGlyLeuMetAlaLeuThrLeuSerProTyrTyrLys  
CGTCGTGTGGCGGTGTTGTTCTCGTCGGGTTGATGGCGCTGACTCTGTACCATATTACA  
GCAGCACACCGCCACAACAAGAGCAGCCCACTACCGCGACTGAGACAGTGGTATAATGT

361 ArgTyrIleSerTrpCysLeuTrpTrpLeuGln  
AGCGCTATATCAGCTGGTGCTTGTGGTGGCTTCAGAA  
TCGCGATATAGTCGACCACGAACACCACCGAAGTCTT

FIG. 25

1 ProAlaProSerGlyCysProProAspSerAspAlaGluSerTyrSerSerMetProPro  
CCAGCCCCCTTCTGGCTGCCCCCCCAGTCCGACGCTGAGTCCTATTCTCCATGCCCCCC  
GGTCGGGGAAGACCGACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGG

61 LeuGluGlyGluProGlyAspProAspLeuSerAspGlySerTrpSerThrValSerSer  
CTGGAGGGGGAGCCTGGGGATCCGGATCTTAGCGACGGGTCATGGTCAACAGTCAGTAGT  
GACCTCCCCCTCGGACCCCTAGGCCTAGAATCGCTGCCAGTACCAGTTGTACGTCATCA

-----Overlap with 33g-----

121 GluAlaAsnAlaGluAspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeu  
GAGGCCAACGCGGAGGATGTCGTGTGCTGCTCAATGTCCTACTCTTGGACAGGCGCACTC  
CTCCGGTTGCGCCTCTACAGCACACGACGAGTTACAGGATGAGAACCTGTCCGCGTGAG

181 ValThrProCysAlaAlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeu  
GTCACCCCGTGCGCCGCGGAAGAACAAGAACTGCCATCAATGCACTGAGCAACTCGTTG  
CAGTGGGGCACGCGGCGCCTTCTTGTCTTTGACGGGTAGTTACGTGACTCGTTGAGCAAC

241 LeuArgHisHisAsnLeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLys  
CTACGTCACCACAATTTGGTGTATTCCACCACCTCACGCACTGCTTGCCAAAGGCAGAAAG  
GATGCAGTGGTGTAAACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTC

301 LysValThrPheAspArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGly  
AAAGTCACATTTGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAG  
TTTCAGTGTAACCTGTCTGACGTTCAAGACCTGTCGGTAATGGTCTGCATGAGTTCTTC

361 ValLysAlaAlaAlaSerLysValLysAlaAsnPhe  
GTTAAAGCAGCGGCGTCAAAAGTGAAGGCTAACTTC  
CAATTTCTGTCGCCGAGTTTTCACTTCCGATTGAAG



FIG. 26A

1      GluTyrValValLeuLeuPheLeuLeuLeuAlaAspAlaArgValCysSerCysLeuTrp  
GGGAGTACGTCGTTCTCCTGTTCTTCTGCTTGCAGACGCGCGCTGCTCCTGCTTGT  
CCCTCATGCAGCAAGAGGACAAGGAAGACGAACGTCTGCGCGCGCAGACGAGGACGAACA

61      MetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsnLeuValIleLeuAsnAla  
GGATGATGCTACTCATATCCCAAGCGGAGGCGGCTTTGGAGAACCTCGTAATACTTAATG  
CCTACTACGATGAGTATAGGGTTCGCCTCCGCCGAAACCTCTTGGAGCATTATGAATTAC

121      AlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuValPhePheCysPheAlaTrp  
CAGCATCCCTGGCCGGGACGCACGGTCTTGATCCTTCCTCGTGTTCTTCTGCTTTGCAT  
GTCGTAGGGACCGGCCCTGCGTGCCAGAACATAGGAAGGAGCACAAGAAGACGAAACGTA

181      TyrLeuLysGlyLysTrpValProGlyAlaValTyrThrPheTyrGlyMetTrpProLeu  
GGTATTTGAAGGGTAAGTGGGTGCCCGGAGCGGTCTACACCTTCTACGGGATGTGGCCTC  
CCATAAATCTCCATTACCCACGGGCCTCGCCAGATGTGGAAGATGCCCTACACCGGAG

241      LeuLeuLeuLeuAlaLeuProGlnArgAlaTyrAlaLeuAspThrGluValAlaAla  
TCCTCCTGCTCCTGTTGGCGTTGCCCGAGCGGCGTACGCGCTGGACACGGAGGTGGCCG  
AGGAGGACGAGGACAACCGCAACGGGGTCCGCCGATGCGCGACCTGTGCTCCACCGGC

301      SerCysGlyGlyValValLeuValGlyLeuMetAlaLeuThrLeuSerProTyrTyrLys  
CGTCGTGTGGCGGTGTTGTTCTCGTCGGGTGATGGCGTGA CTCTGTACCATATTACA  
GCAGCACACCGCCACAACAAGAGCAGCCCACTACCGCGACTGAGACA GTGGTATAATGT

361      ArgTyrIleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeuThrArgValGluAlaGln  
AGCGCTATATCAGCTGGTGCTTGTGGTGGCTTCAGTATTTTCTGACCAGAGTGAAGCGC  
TCGCGATATAGTCGACCACGAACACCACCGAAGTCATAAAGACTGGTCTCACCTTCGCG

421      LeuHisValTrpIleProProLeuAsnValArgGlyGlyArgAspAlaValIleLeuLeu  
AACTGCACGTGTGGATTCCCCCTCAACGTCCGAGGGGGGCGCGACGCCGTCATCTTAC  
TTGACGTGCACACTAAGGGGGGAGTTGCAGGCTCCCCCGCGCTGCGGCAGTAGAATG

481      MetCysAlaValHisProThrLeuValPheAspIleThrLysLeuLeuLeuAlaValPhe  
TCATGTGTGCTGTACACCCGACTCTGGTATTTGACATCACCAAATTGCTGCTGGCCGTCT  
AGTACACACGACATGTGGGCTGAGACCATAAAGTGTAGTGGTTTAACGACGACCGGCAGA

541      GlyProLeuTrpIleLeuGlnAlaSerLeuLeuLysValProTyrPheValArgValGln  
TCGGACCCCTTTGGATTCTTCAAGCCAGTTTGCTTAAAGTACCCTACTTTGTGCGCGTCC  
AGCCTGGGGAAACCTAAGAAGTTCGGTCAAACGAATTTATG6GATGAAACACGCGCAGG

601      GlyLeuLeuArgPheCysAlaLeuAlaArgLysMetIleGlyGlyHisTyrValGlnMet  
AAGGCTTCTCCGGTTCTGCGCGTTAGCGCGGAAGATGATCGGAGGCCATTACGTGCAAA  
TTCCGGAAGAGGCCAAGACGCGCAATCGCGCCTTCTACTAGCCTCCGGTAATGCACGTTT

661      ValIleIleLysLeuGlyAlaLeuThrGlyThrTyrValTyrAsnHisLeuThrProLeu  
TGGTCATCATTAAGTTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCACTCCTC  
ACCAAGTAGTAATTCAATCCCCGCAATGACCGTGGATACAAATATTGGTAGAGTGAGGAG

721      ArgAspTrpAlaHisAsnGlyLeuArgAspLeuAlaValAlaValGluProValValPhe  
TTCGGGACTGGGCGCACAAACGGCTTGCGAGATCTGGCCGTGGCTGTAGAGCCAGTCGTCT  
AAGCCCTGACCCGCGTGTGCGGAACGCTTAGACC66CACCGACATCTCGGTACAGAGA

781      SerGlnMetGluThrLysLeuIleThrTrpGlyAlaAspThrAlaAlaCysGlyAspIle  
TCTCCCAAATGGAGACCAAGCTCATCAGTGGGGGGCAGATACCGCCGCGTGGGTGACA  
AGAGGGTTTACCTCTG6TTGAGTAGTGACACCCCGTCTATG6GCGCGCACGCCACTGT

841      IleAsnGlyLeuProValSerAlaArgArgGlyArgGluIleLeuLeuGlyProAlaAsp  
TCATCAACGGCTTGCTGTTTCCGCCGCGAGGGGAGATACTGCTCGGGCCAGCCG  
AGTAGTTGCCGAACGGACAAGGCGGGCGTCCCCGGCCCTCTATGACGAGCCG6TG6G

901      GlyMetValSerLysGlyTrpArgLeuLeuAlaProIleThrAlaTyrAlaGlnGlnThr  
ATGGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCCATCACGGCGTACGCCAGACG  
TACCTTACCAGAGGTTCCCCACCTCCAACGACCGCGGGTAGTGCCGCGATGCGGGTCTGTCT



# FIG. 26B

Arg61yLeuLeuGlyCysIlelleThrSerLeuThrGlyArgAspLysAsnGlnValGlu  
961 CAAGGGGCTCCTAGGGTGCATAATCACCAGCCTAACTGGCCGGGACAAAACCAAGTGG  
GTTCCCGGAGGATCCCACGTATTAGTGGTCGGATTGACCGGCCCTGTTTTGGTTCCAC

GlyGluValGlnIleValSerThrAlaAlaGlnThrPheLeuAlaThrCysIleAsnGly  
1021 AGGGTGAGGTCCAGATTGTGTCAACTGCTGCCAAACCTTCTGGCAACGTGCATCAATG  
TCCCACTCCAGGTCTAACACAGTTGACGACGGGTTTGGAAAGGACCGTTGCACGTAGTTAC

ValCysTrpThrValTyrHisGlyAlaGlyThrArgThrIleAlaSerProLysGlyPro  
1081 GGGTGTGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCATCGCGTACCCAAGGGTC  
CCACACGACCTGACAGATGGTGCCCGGGCCTTGTCTCTGGTAGCGCAGTGGGTTCCACG

ValIleGlnMetTyrThrAsnValAspGlnAspLeuValGlyTrpProAlaProGlnGly  
1141 CTGTCATCCAGATGTATACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCCGCAAG  
GACAGTAGGTCTACATATGGTTACATCTGGTTCTGGAACACCCGACCGGGCGAGGGCTTC

SerArgSerLeuThrProCysThrCysGlySerSerAspLeuTyrLeuValThrArgHis  
1201 GTAGCCGCTCATTGACACCCTGCACTTGCGGCTCTCGGACCTTTACCTGGTCACGAGGC  
CATCGCGAGTAACCTGTGGGACGTGAACGCGGAGGAGCTGGAATGGACCAAGTGTCTCG

AlaAspValIleProValArgArgArgGlyAspSerArgGlySerLeuLeuSerProArg  
1261 ACGCCGATGTCAATCCCGTGCAGCGGGCGGGGTGATAGCAGGGGCGAGCTGTGTGCGCCC  
TGGGGCTACAGTAAGGGCACGCGGCCGCCCACTATCGTCCCGTGGACGACAGCGGGG

ProIleSerTyrLeuLysGlySerSerGlyGlyProLeuLeuCysProAlaGlyHisAla  
1321 GGCCCATTTCTACTTGAAAGGCTCCTCGGGGGGTCCGCTGTTGTGCCCGCGGGGACG  
CCGGGTAAAGGATGAACTTTCCGAGGAGCCCCCAGGCGACAACACGGGGCGCCCCGTGC

ValGlyIlePheArgAlaAlaValCysThrArgGlyValAlaLysAlaValAspPheIle  
1381 CCGTGGGCATATTTAGGGCCGCGGTGTGCACCCGTGGAGTGGCTAAGGCGGTGGACTTTA  
GGCACCCGTATAAATCCCGGCGCCACACGTGGGCACCTCACCATTCCGCCACCTGAAAT

ProValGluAsnLeuGluThrThrMetArgSerProValPheThrAspAsnSerSerPro  
1441 TCCTGTGGAGAACCTAGAGACAACCATGAGGTCCCCGGTGTTCACGGATAACTCTCTC  
AGGGACACCTCTTGGATCTCTGTTGGTACTCCAGGGGCCACAAGTGCTATTGAGGAGAG

ProValValProGlnSerPheGlnValAlaHisLeuHisAlaProThrGlySerGlyLys  
1501 CACCAGTAGTGCCCCAGAGCTTCCAGGTGGCTCACCTCCATGCTCCACAGGCGAGCGGCA  
GTGGTCATCACGGGGTCTCGAAGGTCCACCGAGTGGAGGTACGAGGGTGTCCGTGCCGT

SerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsnPro  
1561 AAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAACC  
TTTCGTGGTTCCAGGGCCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAGTTGG

SerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAspPro  
1621 CCTCTGTTGCTGCAACACTGGGCTTGGTGCTTACATGTCCAAGGCTCATGGGATCGATC  
GGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTAG

AsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThrTyr  
1681 CTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCAGTACTCCACCT  
GATTGTAGTCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGGA

GlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleCysAsp  
1741 ACGGCAAGTTCCTTGCCGACGGCGGGGTGCTCGGGGGGCGCTTATGACATAATAATTTGTG  
TGCCGTTCAAGGAACGGCTGCCGCCACGAGCCCCCGGAATACTGTATTATTAAACAC

GluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGlnAla  
1801 ACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCGGCACTGTCTTGACCAAG  
TGCTCACGGTGAGGTGCTACGGTGTAGGTAGAACCCGTAGCCGTGACAGGAACCTGGTTC

GluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerValThr  
1861 CAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC  
GTCTCTGACGCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGGCCGAGGCAAGT

ValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPheTyr  
1921 CTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTTT  
GACACGGGGTAGGGTTGTAGTCTCTCAACGAGACAGGTGGTGGCTCTCTAGGGAAAAA



# FIG. 26C

GlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHisSer  
1981 ACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTCTATT  
TGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCTCTGTAGAGTAGAAGACAGTAA

LysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaValAla  
2041 CAAAGAAGAAGTGCACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTGG  
GTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCACC

TyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValAla  
2101 CCTACTACCGCGGTCTTGACGTGTCCGTATCCCGACCAGCGGCGATGTTGTCGTCTGG  
GGATGATGGCGCCAGAACTGCACAGGCACTAGGGCTGGTCGCCGCTACAAACAGCAGCACC

ThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsnThr  
2161 CAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAATA  
GTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTAT

CysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIleThr  
2221 CGTGTGTACCCAGACAGTCTGATTTACGCTTGACCTACCTTCACCTAGAGACAATCA  
GCACACAGTGGGTCTGTAGCTAAAGTCGGAAGTGGGATGGAAGTGGTAACTCTGTTAGT

LeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLysPro  
2281 CGCTCCCCAGGATGCTGTCTCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGGAAGC  
GCGAGGGGGTCTACGACAGAGGGCGTGAGTTGACGCCCCGTCCTGACCGTCCCCCTTCG

GlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSerVal  
2341 CAGGCATCTACAGATTTGTGGCACCAGGGGAGCGCCCTCCGGCATGTTGCACTCGTCCG  
GTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGGC

LeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThrThr  
2401 TCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCAGGAGACTA  
AGGAGACACTCACGATACTGCGTCCGACACGAACATACTCGAGTGCGGGCGGCTCTGAT

ValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeuGlu  
2461 CAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTTG  
GTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCTGGTAGAAC

PheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGlnThr  
2521 AATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCGAGA  
TTAAACCCCTCCGCGAGAAATGTCCGAGTGAGTATATCTACGGGTGAAAGATAGGGTCT

LysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAlaArg  
2581 CAAAGCAGAGTGGGGAGAACCCTTCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCTA  
GTTTCGTCTACCCCTCTTGGAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGAT

AlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLysPro  
2641 GGGCTCAAGCCCTCCCCATCGTGGGACCAGATGTGGAAGTGTGTTGATTGCGCTCAAGC  
CCCGAGTTCGGGGAGGGGTAGCACCCTGGTCTACACCTTCAAACTAAGCGGAGTTCCG

ThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIleThr  
2701 CCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTTCAAGATGAAATCA  
GGTGGGAGGTACCCGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAGT

LeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluValVal  
2761 CCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCCGACCTGGAGGTCG  
GGGACTGCGTGGGTGAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCTCCAGC

ThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeuSer  
2821 TCACGAGCACTGGGTGCTCGTTGGCGGCGTCTGGCTGCTTTGGCCGCGTATTGCTGT  
AGTGCTCGTGAGCCACGAGCAACCGCCGAGGACCGACGAAACGGCGCATACGGACA

ThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIlePro  
2881 CAACAGGCTGCGTGGTCAATAGTGGGCAAGGTCGTCTTGTCCGGGAAGCGGCAATCATAC  
GTTGTCGACGCACAGTATCACCCGTCCAGCAGAACAGGCCCTTCGGCCGTTAGTATG



# FIG. 26D

TyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeuLeu  
3001 CGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCC  
GCATGTAGCTCGTTCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAGG

GlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGlnLys  
3061 TGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCTGCTGTCCAGACCAACTGGCAAA  
ACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGACGACAGGTCTGGTTGACCGTTT

LeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeuAla  
3121 AACTCGAGACCTTCTGGGCGAAGCATATGTGGAACCTTCATCAGTGGGATACAATACTTGG  
TTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCTATGTTATGAACC

GlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAlaAla  
3181 CGGGCTTGTCAACGCTGCCTGGTAACCCGCCATTGCTTCATTGATGGCTTTTACAGCTG  
GCCGAAACAGTTGCGACGGACCATTTGGGCGGTAACGAAGTAACACCAGAAATGTCGAC

ValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrpVal  
3241 CTGTACCAAGCCCACTAACCACTAGCCAAACCTCCTCTTCAACATATTGGGGGGGTGGG  
GACAGTGGTGGGTGATTGGTGATCGGTTTGGGAGGAGAAAGTTGTATAACCCCCCACC

AlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAlaGly  
3301 TGGCTGCCAGCTCGCCGCCCGGGTGGCTACTGCTTTGTGGGCTGAGGTGCTGAGCTG  
ACCGACGGGTGAGCGGGCGGGGGCCACGGCGATGACGGAACACCCGCGACCGAATCGAC

AlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyrGly  
3361 GCGCCGCCATCGGCAGTGTGGACTGGGGAAGGTCCTCATAGACATCCTTGAGGGGTATG  
CGCGGGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATACT

AlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSerThr  
3421 GCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCTCCA  
CGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGGT

GluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGlyVal  
3481 CGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGCG  
GCCTCCTGGACCAAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG

ValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrpMet  
3541 TGGTCTGTGCAGCAATACTGCGCCGGCAGTGTGGCCGGGCGAGGGGGCAGTGAGTGA  
ACCAGACACGTCGTTATGACGCGGCGGTGAACCGGGCCGCTCCCCGTCACGTCACT

AsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrValPro  
3601 TGAACCGGCTGATAGCCTTCGCTCCCGGGGGAACCATGTTTCCCCACGCACTACGTGC  
ACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCACG

GluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGlnLeu  
3661 CGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAGC  
GCCTCTCGCTACGTGACGCGGCGCAGTGACGGTATGAGTCGTGGAGTGACATTGGGTGCG

LeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySerTrp  
3721 TCCTGAGGCGACTGCACCAAGTGGATAAGCTCGGAGGTGTACCACTCCATGCTCCGGTTCCT  
AGGACTCCGCTGACGTGGTCACTATTGAGCCTCACATGGTGAGGTACGAGGCCAAGGA

LeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeuLys  
3781 GGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTAA  
CCGATTCCCTGTAGACCTGACCTATACGCTCCACAACCTCGCTGAAATTCTGGACCGATT

AlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyrLys  
3841 AAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCTTTGTGCTCTGCCAGCGCGGGTATA  
TTCGATTGAGTACGGTGTGACGCGACCTAGGGGAAACACAGGACGGTTCGCGCCCATAT

GlyValTrpArgValAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIleThr  
3901 AGGGGGTCTGGCGAGTGGACGGCATCATGCACACTCGTGGCACTGTGGAGCTGAGATCA  
TCCCCAGACCGCTCACCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAGT





# FIG. 26E

SerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAlaPro  
4021 GGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCTGCGC  
CCTCACCTGGAAGGGGTAATTACG6ATGTGGTGCCG6GGGACATGGGGGGAAGGACGCG

AsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGlnVal  
4081 CGAACTACACGTTTCGCGCTATGGAGGGGTGTCTGCAGAGGAATATGTGGAGATAAGGACAGG  
GCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATACACCTCTATTCCGTCC

GlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGlnVal  
4141 TGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTCAAATGCCCCGTGCCAGG  
ACCCCTGAAGGTGATGCACTGCCATACTGATGACTGTTAGAGTTTACGGGCACGGTCC

ProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaProPro  
4201 TCCCATCGCCCGAATTTTTACAGAATTGGACGGGGGTGCGCTACATAGGTTTGGC6CCC  
AGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGGG

CysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrProVal  
4261 CCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTAGAGTAGGACTCCACGAATACCCGG  
GGACGTTGCGGAACGACGCCCTCCTCCATAGTAAGTCTCATCTGAGGTGCTTATGGGCC

GlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeuThr  
4321 TAGGGTCGCAATTACCTTGCAGCCGACCGGACGTGGCCGTGTTGACGTCCATGCTCA  
ATCCAGCGTTAATGGAACGCTCGGGCTTGGCTGACCGGCACAACTGCAGGTACGAGT

AspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerProPro  
4381 CTGATCCCTCCCATATAACAGCAGAGGGCGCCGGGCGAAGGTTGGCGAGGGGATCACCCC  
GACTAGGGAGGGTATATTGTCGTCTCCGCCG6CCGCTTCCAACCGCTCCCCTAGTGGGG

SerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCysThr  
4441 CCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTT6CA  
GGAGACACCGGTCGAGGAGCCGATCGGTGATAGGCGAGGTAGAGAGTTCCGTTGAACGT

AlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGlnGlu  
4501 CCGCTAACCATGACTCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGACAGG  
GGCGATTGTAAGTACTGAGGGGACTACGACTCGAGTATCTCCGTTGGAGGATACCTCCGTCC

MetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSerPhe  
4561 AGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCCT  
TCTACCGCCGTTGTAGTGGTCCCACTCAGTCTTTTGTTCACCACTAAGACCTGAGGA

AspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeuArg  
4621 TCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGAGAAATCCTGC  
AGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGATGGGCGTCTTTAGGACG

LysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnProPro  
4681 GGAAGTCTCGGAGATTGCGCCAGGCCCTGCCCCTTGGGCGCGGCGGACTATAACCCCC  
CCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCGGCGCTGATATTGGGGG

LeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysProLeu  
4741 CGCTAGTGGAGACGTGGAAAAAGCCGACTACGAACCACCTGTGGTCCATGGCTGTCCGC  
GCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAAGGTACCGACAGGCG

ProProProLysSerProProValProProProArgLysLysArgThrValValLeuThr  
4801 TTCCACCTCCAAAGTCCCCTCCTGTGCTCCGCTCGGAAGAAGCGGACGGTGGTCTCA  
AAGGTGGAGGTTTCAAGGGAGGACAGGAGGCGGAGCCTTCTTCGCTG6CACCAGGAGT

GluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSerSer  
4861 CTGAATCAACCCTATCTACTGCTTGGCGAGCTCGCCACCAAGCTTTGGCAGCTCCT  
GACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGGA

ThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGlyCys  
4921 CAACTTCCGGCATTACGGGCGACAATACGACAACATCTCTGAGCCCGCCCCCTTCTGGCT  
GTTGAAGCCGTAATGCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAGACCGA

ProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluProGly  
4981 GCCCCCGGACTCCGACGCTGAGTCCTATTCTCCATGCCCCCCTGGAGGGGGAGCCTG  
CGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGAC



FIG. 26F

AspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGluAsp  
5041 GGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAGG  
CCCTAGGCCTAGAATCGCTGCCAGTACCAAGTTGCCAGTCATCACTCCGGTTGCGCCTCC

ValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAlaAla  
5101 ATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCCG  
TACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGGC

GluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsnLeu  
5161 CGGAAGAACAGAACTGCCATCAATGCCTAAGCAACTCGTTGCTACGTACCCACAATT  
GCCTTCTTGCTTTGACGGGTAGTTACGTGATTGTTGAGCAACGATGCAGTGGTGTAA

ValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAspArg  
5221 TGGTGTATTCCACCACCTCACGAGTGCTTGCCAAAGGCGAAGAAAGTCACATTTGACA  
ACCACATAAGGTGGTGGAGTGCCTCACGAACGGTTTCCGTCTTCTTTCAGTGAACTGT

LeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAlaSer  
5281 GACTGCAAGTTCTGGACAGCCATTACAGGACGTACTCAAGGAGGTTAAAGCAGCGGGCT  
CTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCTCCAATTCGTCGCCGCA

LysValLysAlaAsnLeu  
5341 CAAAAGTGAAGGCTAAGTTG  
GTTTTCACTTCCGATTGAAC

FIG. 30

1 GlyGlyGluAsnCysGlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCys  
GGGGGGGAGAACTGCGGCTATCGCAGGTGCCGCGCAAGCGGCGTACTGACAACTAGCTGT  
CCCCCCTCTTGACGCCGATAGCGTCCACGGCGCGTTCGCCGCGTACTGTTGATCGACA

61 GlyAsnThrLeuThrCysTyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGln  
GGTAACACCCTCACTTGTTACATCAAGGCCGAGCAGCCTGTCGAGCCGAGGGCTCCAG  
CCATTGTGGGAGTGAACAATGTAGTTCGGGGCTCGTCGGACAGCTCGGCGTCCCGAGGT

-----Overlap with 19g-----  
121 AspCysThrMetLeuValCysGlyAspLeuValValIleCysGluSerAlaGlyVal  
GACTGCACCATGCTCGTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGT  
CTGACGTGGTACGAGCACACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCAG

181 GlnGluAspAlaAlaSerLeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaPro  
CAGGAGGACGCGGCGAGCCTGAGAGCCTTACGGAAGGCTATGACCAGGTACTCGCCCCC  
GTCTCTCTGCGCGCTCGGACTCTCGGAAGTGCTCCGATACTGGTCCATGAGGCGGGG

241 ProGlyAspProProGlnProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsn  
CCTGGGGACCCCCACAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAAC  
GGACCCTGGGGGGTGTGGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTG

301 ValSerValAlaHisAspGlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThr  
GTGTCAGTCGCCACGACGGCGCTGGAAGAGGGTCTACTACCTACCCGTGACCCTACA  
CACAGTCAGCGGGTGTGCGCGACCTTCTCCAGATGATGGAGTGGGCACTGGGATGT

361 ThrProLeuAlaArgAlaAlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeu  
ACCCCCCTCGCGAGAGCTGCGTGGGAGACAGCAAGACACTCCAGTCAATTCCTGGCTA  
TGGGGGAGCGCTCTCGACGCACCTCTGTGTTCTGTGTGAGGTGAGTTAAGGACCGAT

421 GlyAsnIleIleMetPheAlaProThrLeuTrpAla  
GGCAACATAATCATGTTTGGCCCCACACTGTGGGCG  
CCGTTGTATTAGTACAAACGGGGGTGTGACACCCGC



FIG. 27

IlePheLysIleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsn  
1 CCATATTTAAATCAGGATGTACGTGGAGGGGTGCAACACAGGCTGGAAGCTGCCCTGCA  
GGTATAAATTTAGTCCATGACACCTCCAGCTTGTGTCCGACCTTCGACGGACGT

TrpThrArgGlyGluArgCysAspLeuGluAspArgAspArgSerGluLeuSerProLeu  
61 ACTGGACGGCGGCGAACGTTGCGATCTGGAAGACAGGACAGGTCAGAGCTCAGCCCCGT  
TGACCTGGCCCCCGCTTGCAACGCTAGACCTTCTGTCCCTGTCCAGGCTCGAGTCGGGCA

LeuLeuThrThrThrGlnTrpGlnValLeuProCysSerPheThrThrLeuProAlaLeu  
121 TACTGCTGACCACTACACAGTGGCAGGTCTCCCGTGTCTTCACAACCTTACCAGCCT  
ATGACGACTGGTGATGTGTACCGTCCAGGAGGGCACAAAGGAAGTGTGGGATGGTCCGA

SerThrGlyLeuIleHisLeuHisGlnAsnIleValAspValGlnTyrLeuTyrGlyVal  
181 TGTCCACCGGCTCATCCACCTCCACCCAGAACATTTGGACGTGCAGTACTGTACGGGG  
ACAGGTGGCCGGAGTAGGTGGAGGTGGTCTTGTAAACACCTGCACGTCAATGAACATGCCCC

GlySerSerIleAlaSerTrpAlaIleLysTrpGluTyrValValLeuPheLeuLeu  
241 TGGGGTCAAGCATCGCGTCTGGGCCATTAAAGTGGAGTACGTCTCTCTCTCTCTTC  
ACCCAGTTCGTAGCGCAGGACCCGGTAATTACCCCTCATGCAGCAAGAGGACAAGGAAG

LeuAlaAspAlaArgValCysSerCysLeuTrpMetMetLeuIleSerGlnAlaGlu  
301 TGCTTGACAGACGGCGGTCTGCTCTCTGTGGATGATGCTACTCATATCCCAAGCGG  
ACGAACGTCTGCGCGGCAGACGAGGACGAAACCTACTACGATGATAGGGTTCCGCC

-----Overlap with 14i-----  
AlaAlaLeuGluAsnLeuValIleLeuAsnAlaAlaSerLeuAlaGlyThrHisGlyLeu  
361 AGCGGGCTTTGGAGAACCTCGTAATACTTAATGCAGCATCCCTGGCCGGGACGACGGTC  
TCCGCCGAAACCTCTTGGAGCATTATGAATTACGTCTGAGGACCGGCCCTCGGTGCCAG

-----  
Val  
421 TTGTATC  
AACATAG



FIG. 28

-----Overlap with 39c-----  
LeuLysGluValLysAlaAlaAlaSerLysValLysAlaAsnLeuLeuSerValGluGlu  
1 TGCTCAAGGAGGTTAAAGCAGCGGCGTCAAAGTGAAGGCTAACTTGCTATCCGTAGAGG  
ACGAGTTCCTCCAATTTCTGTCGCCGAGTTTTCACTTCCGATTGAACGATAGGCATCTCC  
  
AlaCysSerLeuThrProProHisSerAlaLysSerLysPheGlyTyrGlyAlaLysAsp  
61 AAGCTTGACGCTGACGCCCCCAGCTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAG  
TTCGAACGTCGGACTGCGGGGGTGTGAGTCGGTTTAGGTTCAAACCAATACCCCGTTTTTC  
  
ValArgCysHisAlaArgLysAlaValThrHisIleAsnSerValTrpLysAspLeuLeu  
121 ACGTCCGTTGCCATGCCAGAAAGGCCGTAAACCACATCAACTCCGTGTGGAAAGACCTTC  
TGCAGGCAACGGTACGGTCTTTCCGGCATTGGGTGTAGTTGAGGCACACCTTTCTGGAAG  
  
GluAspAsnValThrProIleAspThrThrIleMetAlaLysAsnGluValPheCysVal  
181 TGGAAGACAATGTAACACCAATAGACACTACCATCATGGCTAAGAACGAGGTTTTCTGCG  
ACCTTCTGTTACATTGTGGTTATCTGTGATGGTAGTACCGATTCTTGCTCCAAAAGACGC  
  
GlnProGluLysGlyGlyArgLysProAlaArgLeuIleValPheProAspLeuGlyVal  
241 TTCAGCCTGAGAAGGGGGTTCGTAAGCCAGCTCGTCTCATCGTGTCCCGATCTGGGCG  
AAGTCGGACTCTTCCCCCAGCATTCGGTTCGAGCAGAGTAGCACAAGGGGCTAGACCCGC  
  
ArgValCysGluLysMetAlaLeuTyrAspValValThrLysLeuProLeuAlaValMet  
301 TGC GCGTGTGCGAAAAGATGGCTTTGTACGACGTGGTTACAAAGCTCCCTTGGCCGTGA  
ACGCGCACACGCTTTTCTACCGAAACATGCTGCACCAATGTTTCGAGGGGAACCGGCACT  
  
GlySerSerTyrGlyPheGlnTyrSerProGlyGlnArgValGluPheLeuValGlnAla  
361 TGGGAAGCTCCTACGGATTCCAATACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAG  
ACCCTTCGAGGATGCCTAAGGTTATGAGTGGTCTGTCGCCCACTTAAGGAGCACGTTT  
  
TrpLysSerLysLysThrProMetGlyPheSerTyrAspThrArgCysPheAspSerThr  
421 CGTGGAAGTCCAAGAAAACCCCAATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCA  
GCACCTTCAGGTTCTTTGGGGTTACCCCAAGAGCATACTATGGGCGACGAACTGAGGT  
  
ValThrGluSerAspIleArgThrGluGluAla  
481 CAGTCACTGAGAGCGACATCCGTACGGAGGAGGCA  
GTCAGTGA CTCTCGCTGTAGGCATGCCTCCTCCGT



FIG. 29

-----  
1 GluPheLeuValGlnAlaTrpLysSerLysLysThrProMetGlyPheSerTyrAspThr  
GAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATGGGGTTCTCGTATGATACC  
CTTAAGGAGCACGTTTCGCACCTTCAGGTTCTTTTGGGGTTACCCCAAGAGCATACTATGC  
-----Overlap with 35f-----  
61 ArgCysPheAspSerThrValThrGluSerAspIleArgThrGluGluAlaIleTyrGln  
CGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACGGAGGAGGCAATCTACCAA  
GCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGCCTCCTCCGTTAGATGGTT  
121 CysCysAspLeuAspProGlnAlaArgValAlaIleLysSerLeuThrGluArgLeuTyr  
TGTTGTGACCTCGACCCCCAAGCCCGGTGGCCATCAAGTCCCTCACCGAGAGGCTTTAT  
ACAACACTGGAGCTGGGGGTTCCGGCGCACCGGTAGTTCAGGGAGTGCTCTCCGAAATA  
181 ValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGlyTyrArgArgCysArgAla  
GTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGCTATCGCAGGTGCCGCGCG  
CAACCCCCGGGAGAAATGGTTAAGTTCCCCCTCTTGACGCCGATAGCGTCCACGGCGCGC  
241 SerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCysTyrIleLysAlaArgAla  
AGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCACTTGCTACATCAAGGCCCCGGCA  
TCGCCGATGACTGTTGATCGACACCATGTGTTGGAGTGAACGATGTAGTTCCGGGGCCCGT  
301 AlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuValCysGlyAspAspLeuVal  
GCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTGTGTGGCGACGACTTAGTC  
CGGACAGCTCGGCGTCCCGAGGTCTTGACGTGGTACGAGCACACACCGCTGCTGAATCAG  
361 ValIleCysGluSerAlaGlyValGlnGluAspAlaAla  
GTTATCTGTGAAAGCGCGGGGTCCAGGAGGACGCGGCGAG  
CAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCGCTC



FIG. 31

-----  
GlyAlaGlyLysArgValTyrThrLeuThrArgAspProThrThrProLeuAlaArgAla  
CGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCCTACAAACCCCTCGCGAGAGC  
GCCGCGACCTTCTCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGAGCGCTCTCG

-----Overlap with 26g-----  
AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe  
TGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTT  
ACGCACCCCTCTGTCTGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAA

-----  
AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla  
TGCCCCCACACTGTGGCGAGGATGATGATGATGACCCATTCTTTAGCGTCTTATAGC  
ACGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCG

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu  
CAGGGACCCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCCTGCTACTCCATAGA  
GTCCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCCGACGATGAGGTATCT

ProLeuAspLeuProIleIleGlnArgLeu  
ACCACTTGATCTACCTCCAATCATTCAAAGACTC  
TGGTGAACTAGATGGAGGTTAGTAAGTTTCTGAG

1

61

121

181

241



FIG. 32A

IlePheLysIleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsn  
1 CCATATTTAAATCAGGATGTACGTGGGAGGGGTCGAACACAGGCTGGAAGCTGCCTGCA  
GGTATAAATTTAGTCCTACATGCACCCTCCCCAGCTTGTGTCCGACCTTCGACGGACGT

TrpThrArgGlyGluArgCysAspLeuGluAspArgAspArgSerGluLeuSerProLeu  
61 ACTGGACGCGGGGCGAACGTTGCGATCTGGAAGACAGGGACAGGTCCGAGCTCAGCCCGT  
TGACCTGCGCCCCGCTTGCAACGCTAGACCTTCTGTCCCTGTCCAGGCTCGAGTCGGGCA

LeuLeuThrThrThrGlnTrpGlnValLeuProCysSerPheThrThrLeuProAlaLeu  
121 TACTGCTGACCACTACACAGTGGCAGGTCTCCCGTGTTCTTCACAACCTACCAGCCT  
ATGACGACTGGTGATGTGTACCCTCCAGGAGGGCACAAGGAAGTGTGGGATGGTCGGA

SerThrGlyLeuIleHisLeuHisGlnAsnIleValAspValGlnTyrLeuTyrGlyVal  
181 TGTCCACCGGCTCATCCACCTCCACCAGAACATTGTGGACGTGCAGTACTTGTACGGGG  
ACAGGTGGCCGGAGTAGGTGGAGGTGGTCTTGTAAACCTGCACGTGATGAACATGCCCC

GlySerSerIleAlaSerTrpAlaIleLysTrpGluTyrValValLeuLeuPheLeuLeu  
241 TGGGGTCAAGCATCGCGTCCTGGGCCATTAAAGTGGGAGTACGTCGTTCTCTGTTCTTCTC  
ACCCAGTTCGTAGCGCAGGACCCGGTAATTCACCCTCATGCAGCAAGAGGACAAGGAAG

LeuAlaAspAlaArgValCysSerCysLeuTrpMetMetLeuLeuIleSerGlnAlaGlu  
301 TGCTTGACAGCGCGCGCTGCTGCTGCTTGTGGATGATGCTACTCATATCCCAAGCGG  
ACGAACGTCTGCGCGCGCAGACGAGGACGAACACCTACTACGATGAGTATAGGGTTCGCC

AlaAlaLeuGluAsnLeuValIleLeuAsnAlaAlaSerLeuAlaGlyThrHisGlyLeu  
361 AGGCGGCTTTGGAGAACCTCGTAATACTTAATGCAGCATCCCTGGCCGGGACGCACGGTC  
TCCGCCGAAACCTCTTGAGCATTATGAATTACGTCGTAGGGACCGGCCCTGCGTGCCAG

ValSerPheLeuValPhePheCysPheAlaTrpTyrLeuLysGlyLysTrpValProGly  
421 TTGTATCCTTCCTCGTGTCTTCTGCTTTGCATGGTATTTGAAGGGTAAGTGGGTGCCCC  
AACATAGGAAGGAGCACAAGAAGACGAAACGTACCATAAACTTCCCATTACCCACGGGG

AlaValTyrThrPheTyrGlyMetTrpProLeuLeuLeuLeuLeuAlaLeuProGln  
481 GAGCGGTCTACACCTTCTACGGGATGTGGCCTCTCTCTGCTCTGTTGGCGTTGCCCC  
CTCGCCAGATGTGGAAGATGCCCTACACCGGAGAGGAGGACGAGGACAACCGCAACGGGG

ArgAlaTyrAlaLeuAspThrGluValAlaAlaSerCysGlyGlyValValLeuValGly  
541 AGCGGGCGTACGCGCTGGACACGGAGGTGGCCGCGTCGTGTGGCGGTGTTGTTCTCGTCG  
TCGCCCCGATGCGCGACCTGTGCCTCCACCGGCGCAGCACACCGCCACAACAAGAGCAGC

LeuMetAlaLeuThrLeuSerProTyrTyrLysArgTyrIleSerTrpCysLeuTrpTrp  
601 GGTGATGGCGCTGACTCTGTCAACATATTACAAGCGCTATATCAGCTGGTGTGTTGTGGT  
CCAACTACCGCGACTGAGACAGTGGTATAATGTTGCGATATAGTCGACCACGAACACCA

LeuGlnTyrPheLeuThrArgValGluAlaGlnLeuHisValTrpIleProProLeuAsn  
661 GGCTTCAGTATTTTCTGACCAGAGTGGAGCGCAACTGCACGTGTGGATTCCCCCCTCA  
CCGAAGTCATAAAAGACTGGTCTCACCTTCGCGTTGACGTGCACACCTAAGGGGGGGAGT

ValArgGlyGlyArgAspAlaValIleLeuLeuMetCysAlaValHisProThrLeuVal  
721 ACGTCCGAGGGGGGCGCGACGCCGTCTTACTCATGTGTGCTGTACACCCGACTCTGG  
TGCAGGCTCCCCCGCGCTGCGGCAGTAGAATGAGTACACACGACATGTGGGCTGAGACC

PheAspIleThrLysLeuLeuLeuAlaValPheGlyProLeuTrpIleLeuGlnAlaSer  
781 TATTTGACATCACAAATTGCTGCTGGCCGTCTTCGGACCCCTTTGGATTCTTCAAGCCA  
ATAAACTGTAGTGGTTTAAACGACGACCGGCAGAGCCTGGGGAAACCTAAGAAGTTCGGT

LeuLeuLysValProTyrPheValArgValGlnGlyLeuLeuArgPheCysAlaLeuAla  
841 GTTTGCTTAAAGTACCCTACTTTGTGCGCGTCCAAGGCCCTTCTCCGGTTCTGCGCGTTAG  
CAAACGAATTTTCATGGGATGAAACACGCGCAGGTTCCGGAAGAGGCCAAGACGCGCAATC



FIG. 32B

ArgLysMetIleGlyGlyHisTyrValGlnMetValIleIleLysLeuGlyAlaLeuThr  
901 CGCGGAAGATGATCGGAGGCCATTACGTGCAAATGGTCATCATTAAAGTTAGGGGCGCTTA  
GCGCCTTCTACTAGCCTCCGGTAATGCACGTTTACCAGTAGTAATTCAATCCCCGCGAAT

GlyThrTyrValTyrAsnHisLeuThrProLeuArgAspTrpAlaHisAsnGlyLeuArg  
961 CTGGCACCTATGTTTATAACCATCTCACTCCTCTTCGGGACTGGGCGCACAAACGGCTTGC  
GACCGTGGATACAAATATTGGTAGAGTGAGGAGAAGCCCTGACCCGCGTGTTCGCGAACG

AspLeuAlaValAlaValGluProValValPheSerGlnMetGluThrLysLeuIleThr  
1021 GAGATCTGGCCGTGGCTGTAGAGCCAGTCGTCCTCTCCCAAATGGAGACCAAGCTCATCA  
CTCTAGACCGGCACCGACATCTCGGTCAGCAGAAGAGGGTTTACCTCTGGTTCGAGTAGT

TrpGlyAlaAspThrAlaAlaCysGlyAspIleIleAsnGlyLeuProValSerAlaArg  
1081 CGTGGGGGGCAGATACCGCCGCGTGCCTGACATCATCAACGGCTTGCCTGTTTCCGCCC  
GCACCCCCGTCTATGGCGGCGCACGCCACTGTAGTAGTTGCCGAACGGACAAAGGCGGG

ArgGlyArgGluIleLeuLeuGlyProAlaAspGlyMetValSerLysGlyTrpArgLeu  
1141 GCAGGGGCCGGGAGATACTGCTCGGGCCAGCCGATGGAATGGTCTCCAAGGGGTGGAGGT  
CGTCCCCGGCCCTCTATGACGAGCCCGGTGCGCTACCTTACCAGAGGTTCCCCACCTCCA

LeuAlaProIleThrAlaTyrAlaGlnGlnThrArgGlyLeuLeuGlyCysIleIleThr  
1201 TGCTGGCGCCCATCACGGCGTACGCCAGCAGACAAGGGGCTCCTAGGGTGCATAATCA  
ACGACCGCGGGTAGTGCCGCATGCGGGTCGTCTGTTCCCGGAGGATCCCACGTATTAGT

SerLeuThrGlyArgAspLysAsnGlnValGluGlyGluValGlnIleValSerThrAla  
1261 CCAGCCTAACTGGCCGGGACAAAAACCAAGTGGAGGGTGAGGTCCAGATTGTGTCAACTG  
GGTCGGATTGACCGGCCCTGTTTTTGGTTACCTCCCACTCCAGGTCTAACACAGTTGAC

AlaGlnThrPheLeuAlaThrCysIleAsnGlyValCysTrpThrValTyrHisGlyAla  
1321 CTGCCCAAACCTTCTGGCAACGTGCATCAATGGGGTGTGCTGGACTGTCTACCACGGGG  
GACGGGTTTGGAAGGACCGTTGCACGTAGTTACCCACACGACCTGACAGATGGTGCCCC

GlyThrArgThrIleAlaSerProLysGlyProValIleGlnMetTyrThrAsnValAsp  
1381 CCGGAACGAGGACCATCGCGTCACCCAAGGGTCCTGTTCATCCAGATGTATACCAATGTAG  
GGCCTTGCTCCTGGTAGCGCAGTGGGTTCCAGGACAGTAGGTCTACATATGTTTACATC

GlnAspLeuValGlyTrpProAlaProGlnGlySerArgSerLeuThrProCyrThrCys  
1441 ACCAAGACCTTGTGGGCTGGCCCGCTCCGCAAGGTAGCCGCTCATTGACACCCTGCACTT  
TGGTTCTGGAACACCCGACCGGGCGAGGCGTTCCATCGGCGAGTAAGTGTGGGACGTGAA

GlySerSerAspLeuTyrLeuValThrArgHisAlaAspValIleProValArgArgArg  
1501 GCGGCTCCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATTCCCGTGCGCCGGC  
CGCCGAGGAGCCTGGAAATGGACCAAGTGTCCGTGCGGCTACAGTAAGGGCACGCGGGCCG

GlyAspSerArgGlySerLeuLeuSerProArgProIleSerTyrLeuLysGlySerSer  
1561 GGGGTGATAGCAGGGGCAGCCTGCTGTGCCCCGGGCCATTTCTACTTGAAAGGCTCCT  
CCCCACTATCGTCCCCGTGCGACGACAGCTGGGCCGGGTAAAGGATGAAGTTTCCGAGGA

GlyGlyProLeuLeuCysProAlaGlyHisAlaValGlyIlePheArgAlaAlaValCys  
1621 CGGGGGGTCCGCTGTTGTGCCCCGCGGGGCACGCCGTGGGCATATTTAGGGCCGCGGTGT  
GCCCCCAGGCGACAACACGGGGCGCCCCGTGCGGCACCCGTATAAATCCCGGCGCCACA

ThrArgGlyValAlaLysAlaValAspPheIleProValGluAsnLeuGluThrThrMet  
1681 GCACCCGTGGAGTGGCTAAGGCGGTGGACTTTATCCCTGTGGAGAACCTAGAGACAACCA  
CGTGGGCACCTACCGATTCCGCCACCTGAAATAGGGACACCTCTTGGATCTCTGTTGGT





# FIG. 32C

ArgSerProValPheThrAspAsnSerSerProProValValProGlnSerPheGlnVal  
1741 TGAGGTCCCCGGTGTTCACGGATAACTCCTCTCCACCAGTAGTGCCCCAGAGCTTCCAGG  
ACTCCAGGGGCCACAAGTGCCATTGAGGAGAGGTGGTCATCACGGGGTCTCGAAGGTCC

AlaHisLeuHisAlaProThrGlySerGlyLysSerThrLysValProAlaAlaTyrAla  
1801 TGGCTCACCTCCATGCTCCACAGGCAGCGCAAAAGCACCAAGGTCCCGGTGCATATG  
ACCGAGTGGAGGTACGAGGGTGTCCGTGCGCGTTTTCTGTTCCAGGGCCGACGTATAC

AlaGlnGlyTyrLysValLeuValLeuAsnProSerValAlaAlaThrLeuGlyPheGly  
1861 CAGCTCAGGGCTATAAGGTGCTAGTACTCAACCCCTCTGTTGCTGCAACACTGGGCTTTG  
GTCGAGTCCCGATATTCCACGATCATGAGTTGGGGAGACAACGACGTTGTGACCCGAAAC

AlaTyrMetSerLysAlaHisGlyIleAspProAsnIleArgThrGlyValArgThrIle  
1921 GTGCTTACATGTCCAAGGCTCATGGGATCGATCCTAACATCAGGACCGGGGTGAGAACAA  
CACGAATGTACAGGTTCCGAGTACCCTAGCTAGGATTGTAGTCTGCCCCACTCTTGT

ThrThrGlySerProIleThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCys  
1981 TTACCACTGGCAGCCCCATCACGTACTCCACCTACGGCAAGTTCCTTGCCGACGGCGGGT  
AATGGTGACCGTCGGGGTAGTGATGAGGTGGATGCGGTTCAAGGAACGGCTGCCGCCCA

SerGlyGlyAlaTyrAspIleIleIleCysAspGluCysHisSerThrAspAlaThrSer  
2041 GCTCGGGGGGCGCTTATGACATAATAATTTGTGACGAGTGCCACTCCACGGATGCCACAT  
CGAGCCCCCGCAATACTGTATTATTAACACTGCTACGGTGAGGTGCCTACGGTGTA

IleLeuGlyIleGlyThrValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValVal  
2101 CCATCTTGGGCATCGGCACTGTCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTTG  
GGTAGAACCCGTAGCCGTGACAGGAAGTGGTTCGTCTGACGCCCCGCTCTGACCAAC

LeuAlaThrAlaThrProProGlySerValThrValProHisProAsnIleGluGluVal  
2161 TGCTCGCCACCGCCACCCCTCCGGGCTCCGTCACGTGTGCCCCATCCCAACATCGAGGAGG  
ACGAGCGGTGGCGGTGGGGAGGCCCGAGGCAGTGACACGGGGTAGGGTTGTAGCTCTCC

AlaLeuSerThrThrGlyGluIleProPheTyrGlyLysAlaIleProLeuGluValIle  
2221 TTGCTCTGTCCACCACCGGAGAGATCCCTTTTTACGGCAAGGCTATCCCCCTCGAAGTAA  
AACGAGACAGGTGGTGGCCTCTCTAGGGAAAAATGCCGTTCCGATAGGGGGAGCTTCATT

LysGlyGlyArgHisLeuIlePheCysHisSerLysLysLysCysAspGluLeuAlaAla  
2281 TCAAGGGGGGGAGACATCTCATCTTCTGTCATTCAAAGAAGAAGTGCGACGAAGCTCGCCG  
AGTTCCCCCCTCTGTAGAGTAGAAGACAGTAAGTTTCTTCTTCACGCTGCTTGAGCGGC

LysLeuValAlaLeuGlyIleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerVal  
2341 CAAAGCTGGTCGATTGGGCATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGTCCG  
GTTTCGACCAGCGTAACCCGTAGTTACGGCACCGGATGATGGCGCCAGAAGTGCACAGGC

IleProThrSerGlyAspValValValValAlaThrAspAlaLeuMetThrGlyTyrThr  
2401 TCATCCCGACCAAGCGCGATGTTGTGTCGTGGCAACCGATGCCCTCATGACCGGTATA  
AGTAGGGCTGGTCGCCGCTACAACAGCAGCACCCTGGCTACGGGAGTACTGGCCGATAT

GlyAspPheAspSerValIleAspCysAsnThrCysValThrGlnThrValAspPheSer  
2461 CCGGCGACTTCGACTCGGTGATAGACTGCAATACGTGTGTACCCAGACAGTCGATTTCA  
GGCCGCTGAAGCTGAGCCACTATCTGACGTTATGCACACAGTGGGTCTGTACGCTAAAGT

LeuAspProThrPheThrIleGluThrIleThrLeuProGlnAspAlaValSerArgThr  
2521 GCCTTGACCCTACCTTACCATTGAGACAATCACGCTCCCCAGGATGCTGTCTCCGCA  
CGGAAGTGGGATGGAAGTGGTAAGTCTGTTAGTGCGAGGGGGTCTACGACAGAGGGCGT

GlnArgArgGlyArgThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGly  
2581 CTCAACGTCGGGGCAGGACTGGCAGGGGGAAAGCCAGGCATCTACAGATTTGTGGCACCGG  
GAGTTGACGCCCGTCTGACCGTCCCCCTCCGGTCCGTAGATGTCTAAACACCGTGGCC

GluArgProSerGlyMetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCys  
2641 GGGAGCGCCCCCTCCGGCATGTTGCACTCGTCCGTCTCTGTGAGTGCTATGACGAGGGT  
CCCTCGGGGGAGGCCGTACAAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGA

AlaTrpTyrGluLeuThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThr  
2701 GTGCTTGGTATGAGCTCACGCCCGCCGAGACTACAGTTAGGCTACGAGCGTACATGAACA  
CACGAACCATACTCGAGTGCGGGCGGCTCTGATGTCAATCCGATGCTCGCATGTACTTGT



FIG. 32D

ProGlyLeuProValCysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeu  
2761 CCCCAGGGCTTCCCGTGTGCCAGGACCATCTTGAATTTTGGGAGGGCGTCTTTACAGGCC  
GGGGCCCCGAAGGGCACACGGTCTGTTAGAACTTAAACCCTCCCGCAGAAATGTCCGG

ThrHisIleAspAlaHisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyr  
2821 TCACTCATATAGATGCCACTTTCTATCCAGACAAAGCAGAGTGGGGAGAACCTTCTCT  
AGTGAGTATATCTACGGGTGAAAGATAGGGTCTGTTCTGCTCACCCCTCTTGAAGGAA

LeuValAlaTyrGlnAlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAsp  
2881 ACCTGGTAGCGTACCAAGCCACCGTGTGCGCTAGGGCTCAAGCCCTCCCCATCGTGGG  
TGGACCATCGCATGGTTCGGTGGCACACGCGATCCCGAGTTCCGGGAGGGGGTAGCACCC

GlnMetTrpLysCysLeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeu  
2941 ACCAGATGTGGAAGTGTGTTGATTGCGCTCAAGCCACCTCCATGGGCCAACCCCTGC  
TGGTCTACACCTTCAAACTAAGCGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACG

TyrArgLeuGlyAlaValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIle  
3001 TATACAGACTGGGCGCTGTTCAAGATGAAATCACCTGACGCACCCAGTACCAAATACA  
ATATGTCTGACCCGCGACAAGTCTTACTTTAGTGGGACTGCGTGGGTCAGTGGTTTATGT

MetThrCysMetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGly  
3061 TCATGACATGCATGTGCGCCGACCTGGAGGTCTGACGAGCACCTGGGTGCTCGTTGGCG  
AGTACTGTACGTACAGCCGGCTGGACCTCCAGCAGTGTCTGTTGGACCCACGAGCAACCGC

ValLeuAlaAlaLeuAlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArg  
3121 GCGTCTGGCTGCTTTGGCCGCGTATTGCTGTCAACAGGCTGCGTGGTCATAGTGGGCA  
CGCAGGACCGACGAAACCGGCGCATAACGGACAGTTGTCCGACGCACCAATATCACCCGT

ValValLeuSerGlyLysProAlaIleIleProAspArgGluValLeuTyrArgGluPhe  
3181 GGGTCGTCTTGTCCGGGAAGCCGGCAATCATACCTGACAGGGAAGTCTCTACCGAGAGT  
CCCAGCAGAACAGGCCCTTCGGCCGTAGTATGGACTGTCCCTTCAGGAGATGGCTCTCA

AspGluMetGluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAla  
3241 TCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCG  
AGTACTCTACCTTCTCAGGAGAGTCTGTAATGGCATGTAGCTCGTTCCTACTACGAGC

GluGlnPheLysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluVal  
3301 CCGAGCAGTTCAAGCAGAAAGCCCTCGGCCCTCTGACAGACCGCTCCCGTCAGGCAGAGG  
GGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCC

IleAlaProAlaValGlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMet  
3361 TTATCGCCCTGCTGTCCAGACCAACTGGCAAACTCAGACCTTCTGGGCGAAGCATA  
AATAGCGGGGACGACAGGTCTGGTTGACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTAT

TrpAsnPheIleSerGlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnPro  
3421 TGTGGAACCTTCATCAGTGGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACC  
ACACCTTGAAGTAGTCACCTATGTTATGAACCGCCGACAGTTGCGACGGACCATGG

AlaIleAlaSerLeuMetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGln  
3481 CCGCCATTGCTTCATTGATGGCTTTTACAGCTGCTGTACACAGCCCACTAACCACTAGCC  
GGCGGTAACGAAGTAACACCGAAAATGTCGACGACAGTGGTGGGTGATTGGTGATCGG

ThrLeuLeuPheAsnIleLeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAla  
3541 AAACCTCCTCTTCAACATATTGGGGGGGTGGGTGGCTGCCAGCTCGCCGCCCCGGTG  
TTTGGGAGGAGAAGTTGTATAACCCCCCAACCCACCGACGGGTGAGCGGGGGGGGCCAC

AlaThrAlaPheValGlyAlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGly  
3601 CCGCTACTGCTTTGTGGGCGCTGGCTTAGCTGGCGCGCCATCGGCAAGTGTGGACTGG  
GGCGATGACGGAAACACCCGCGACCGAATCGACCGCGGCGGTAGCCGTCACAACCTGACC

LysValLeuIleAspIleLeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAla  
3661 GGAAGGTCTCATAGACATCCTTGCAGGGTATGGCGCGGGCTGGCGGGAGCTCTTGTGG  
CCTTCCAGGAGTATCTGTAGGAACGTCCCATACCGCGCCGACCGCCCTCGAGAACC

PheLysIleMetSerGlyGluValProSerThrGluAspLeuValAsnLeuLeuProAla  
3721 CATTCAAGATCATGAGCGGTGAGGTCCCTCCACGAGGACCTGGTCAATCTACTGCCCG  
GTAAGTTCTAGTACTGCCACTCCAGGGGAGGTGCCTCTGGACCAAGTTAGATGACGGGG



# FIG. 32E

IleLeuSerProGlyAlaLeuValValGlyValValCysAlaAlaIleLeuArgArgHis  
3781 CCATCCTCTCGCCCGGAGCCCTCGTAGTCGGCGTGGTCTGTGCAGCAATACTGCGCCGGC  
GGTAGGAGAGCGGGCCTCGGGAGCATCA6CCGCACAGACACGTCGTTATGACGCGGGCCG

ValGlyProGlyGluGlyAlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArg  
3841 ACGTTGGCCCGGGCGAGGGGCGAGTGCAGTGGATGAACCGGCTGATAGCCTTCGCTCC  
TGCAACCGGGCCGCTCCCCGTCACGTACCTACTTGGCCGACTATCGGAAGCGGAGGG

GlyAsnHisValSerProThrHisTyrValProGluSerAspAlaAlaAlaArgValThr  
3901 GGGGGAACCATGTTTCCCCACGCACTACGTGCCGGAGAGCGATGCACTGCCCCGCTCA  
CCCCCTGGTACAAAGGGGGTGCCTGATGCACGGCCTCTCGCTACGTGACGGGGCGAGT

AlaIleLeuSerSerLeuThrValThrGlnLeuLeuArgArgLeuHisGlnTrpIleSer  
3961 CTGCCATACTCAGCAGCCTCACTGTAACCCAGCTCCTGAGGCGACTGCACAGTGGATAA  
GACGGTATGAGTCGTGCGAGTGACATTGGGTGAGGACTCCGCTGACGTGGTCACCTATT

SerGluCysThrThrProCysSerGlySerTrpLeuArgAspIleTrpAspTrpIleCys  
4021 GCTCGGAGTGTACCACTCCATGCTCCGGTTCTGGCTAAGGGACATCTGGGACTGGATAT  
CGAGCCTCACATGGTGAGGTACGAGGCCAAGGACCGATTCCCTGTAGACCCTGACCTATA

GluValLeuSerAspPheLysThrTrpLeuLysAlaLysLeuMetProGlnLeuProGly  
4081 GCGAGGTGTTGAGCGACTTTAAGACCTGGCTAAAAGCTAAGCTCATGCCACAGCTGCCTG  
CGTCCACAACCTCGCTGAAATTCGGACCGATTTTCGATTGAGTACGGTGTGACGGAC

IleProPheValSerCysGlnArgGlyTyrLysGlyValTrpArgValAspGlyIleMet  
4141 GGATCCCCTTTGTGCTCTGCCAGCGCGGGTATAAGGGGGTCTGGCGAGTGGACGGCATCA  
CCTAGGGGAAACACAGGACGGTGCGCCCATATTCCCCAGACCGCTCACCTGCCGTAGT

HisThrArgCysHisCysGlyAlaGluIleThrGlyHisValLysAsnGlyThrMetArg  
4201 TGCACACTCGCTGCCACTGTGGAGCTGAGATCACTGGACATGTCAAAAACGGGACGATGA  
ACGTGTGAGCGACGGTGACACCTGACTCTAGTGACCTGTACAGTTTGGCCCTGCTACT

IleValGlyProArgThrCysArgAsnMetTrpSerGlyThrPheProIleAsnAlaTyr  
4261 GGATCGTCGGTCTAGGACCTGCAGGAACATGTGGAGTGGGACCTTCCCCATTAATGCCT  
CCTAGCAGCCAGGATCCTGGACGTCTTGTACACCTACCCCTGGAAGGGGTAATTACGGA

ThrThrGlyProCysThrProLeuProAlaProAsnTyrThrPheAlaLeuTrpArgVal  
4321 ACACCACGGGCCCCTGTACCCCCCTTCTGCGCCGAACCTACACGTTGCGCTATGGAGGG  
TGTGGTGGCCGGGGACATGGGGGGAAGGACGCGGCTTGTGTGCAAGCGCGATACCTCC

SerAlaGluGluTyrValGluIleArgGlnValGlyAspPheHisTyrValThrGlyMet  
4381 TGTCTGCAGAGGAATATGTGGAGATAAGGCAAGGTGGGGGACTTCCACTACGTGACGGGTA  
ACAGACGTCTCCTTATACACCTCTATTCCGTCCACCCCTGAAGGTGATGCACTGCCCAT

ThrThrAspAsnLeuLysCysProCysGlnValProSerProGluPhePheThrGluLeu  
4441 TGACTACTGACAATCTCAAATGCCCGTGGCAGGTCCCATCGCCGAAATTTTACAGAAT  
ACTGATGACTGTTAGAGTTTACGGGCACGGTCCAGGGTAGCGGGCTTAAAGGTGCTTTA

AspGlyValArgLeuHisArgPheAlaProProCysLysProLeuArgGluGluVal  
4501 TGGACGGGGTGCGCCCTACATAGGTTTGCGCCCCCTGCAAGCCCTTGTGCGGGAGGAGG  
ACCTGCCCCACGCGGATGTATCCAAACGCGGGGGGACGTTGCGGAACGACGCCCTCTCC

SerPheArgValGlyLeuHisGluTyrProValGlySerGlnLeuProCysGluProGlu  
4561 TATCATTAGAGTAGGACTCCACGAATACCCGGTAGGGTCGCAATTACCTTGCAGGCCG  
ATAGTAAGTCTCATCCTGAGGTGCTTATGGGCCATCCAGCGTTAATGGAACGCTCGGGC

ProAspValAlaValLeuThrSerMetLeuThrAspProSerHisIleThrAlaGluAla  
4621 AACCGGACGTGGCCGTGTTGACGTCCATGCTCACTGATCCCTCCCATATAACAGCAGAGG  
TTGGCTGCACCGGCACAACTGCAGGTACGAGTGACTAGGGAGGGTATATTGTGCTCTCC

AlaGlyArgArgLeuAlaArgGlySerProProSerValAlaSerSerSerAlaSerGln  
4681 CGGCCGGGCGAAGGTTGGCGAGGGGATACCCCCCTCTGTGGCCAGCTCCTCGGCTAGCC  
GCCGGCCCGCTTCAACCGCTCCCCTAGTGGGGGAGACACCGGTCGAGGAGCCGATCGG

LeuSerAlaProSerLeuLysAlaThrCysThrAlaAsnHisAspSerProAspAlaGlu  
4741 AGCTATCCGCTCCATCTCTCAAGGCACTTGCACCGCTAACCATGACTCCCTGATGCTG  
TCGATAGGCGAGGTAGAGAGTTCCGTTGACGTGGCGATTGGTACTGAGGGGACTACGAC



# FIG. 32F

LeuIleGluAlaAsnLeuLeuTrpArgGlnGluMetGlyGlyAsnIleThrArgValGlu  
4801 AGCTCATAGAGGCCAACCTCCTATGGAGGCAGGAGATGGGCGGCAACATCACCAGGGTTG  
TCGAGTATCTCCGGTTGGAGGATACCTCCGTCTCTACCCGCCGTTGAGTGGTCCCAAC

SerGluAsnLysValValIleLeuAspSerPheAspProLeuValAlaGluGluAspGlu  
4861 AGTCAGAAAACAAAGTGGTGATTCTGGACTCCTTCGATCCGCTTGTGGCGGAGGAGGACG  
TCAGTCTTTTGTTCACCACTAAGACCTGAGGAAGCTAGGCGAACACCGCCTCCTCCTGC

ArgGluIleSerValProAlaGluIleLeuArgLysSerArgArgPheAlaGlnAlaLeu  
4921 AGCGGGAGATCTCCGTACCCGAGAAATCCTGCGGAAGTCTCGGAGATTCGCCAGGCC  
TCGCCCTCTAGAGGCATGGGCGTCTTTAGGACGCCTTCAGAGCCTCTAAGCGGGTCCGGG

ProValTrpAlaArgProAspTyrAsnProProLeuValGluThrTrpLysLysProAsp  
4981 TGCCCGTTTGGGCGCGGCCGACTATAACCCCCGCTAGTGGAGAGCTGGAAAAAGCCG  
ACGGGCAAACCCGCGCGCCGCTGATATTGGGGGGCGATCACCTTGACCTTTTTTCGGG

TyrGluProProValValHisGlyCysProLeuProProProLysSerProProValPro  
5041 ACTACGAACCACTGTGGTCCATGGCTGTCCGCTTCCACCTCCAAAGTCCCTCCTGTGC  
TGATGCTTGGTGGACACCAAGGTACCGACAGGCGAAGGTGGAGGTTTCAGGGGAGGACACG

ProProArgLysLysArgThrValValLeuThrGluSerThrLeuSerThrAlaLeuAla  
5101 CTCCGCCTCGAAGAAGCGGACGGTGGTCTCACTGAATCAACCTATCTACTGCCTTGG  
GAGGCGGAGCCTTCTTCGCTGCCACCAAGAGTGACTTAGTTGGGATAGATGACGGAACC

GluLeuAlaThrArgSerPheGlySerSerSerThrSerGlyIleThrGlyAspAsnThr  
5161 CCGAGCTCGCCACCAGAAAGCTTTGGCAGCTCCTCAACTTCCGGCATTACGGGCGACAATA  
GGCTCGAGCGGTGGTCTTCGAAACCGTCGAGGAGTTGAAGGCCGTAATGCCGCTGTTAT

ThrThrSerSerGluProAlaProSerGlyCysProProAspSerAspAlaGluSerTyr  
5221 CGACAACATCCTCTGAGCCCGCCCTTCTGGCTGCCCGCCGACTCCGACGCTGAGTCCT  
GCTGTTGTAGGAGACTCGGGCGGGGAAGACCGACGGGGGGGCTGAGGCTGCGACTCAGGA

SerSerMetProProLeuGluGlyGluProGlyAspProAspLeuSerAspGlySerTrp  
5281 ATTCTCCATGCCCCCTGGAGGGGGAGCCTGGGGATCCGGATCTTAGCGACGGGTCTAT  
TAAGGAGGTACGGGGGGGACCTCCCCCTCGGACCCTAGGCCCTAGAATCGTGCCCAAGTA

SerThrValSerSerGluAlaAsnAlaGluAspValValCysCysSerMetSerTyrSer  
5341 GGTCAACGGTCAGTAGTGAGGCCAACGCGGAGGATGTCGTGTGCTGCTCAATGTCTTACT  
CCAGTTGCCAGTCATCACTCCGGTTGCGCCTCCTACAGCACACGACGAGTTACAGAATGA

TrpThrGlyAlaLeuValThrProCysAlaAlaGluGluGlnLysLeuProIleAsnAla  
5401 CTTGGACAGGCGCACTCGTCACCCCGTGCGCCGCGGAAGAACAAGAACTGCCCATCAATG  
GAACCTGTCCGCGTGAGCAGTGGGGCACGCGGCGCCTTCTTGTCTTTGACGGGTAGTTAC

LeuSerAsnSerLeuLeuArgHisHisAsnLeuValTyrSerThrThrSerArgSerAla  
5461 CACTAAGCAACTCGTTGCTACGTACCCACAATTTGGTGTATTCCACCACCTACGCGAGTG  
GTGATTGTTGAGCAACGATGCAGTGGTGTAAACCACATAAGGTGGTGGAGTGCGTCAC

CysGlnArgGlnLysLysValThrPheAspArgLeuGlnValLeuAspSerHisTyrGln  
5521 CTTGCCAAAGGCAGAAGAAAGTCACATTTGACAGACTGCAAGTTCTGGACAGCCATTACC  
GAACGGTTTCCGTCTTCTTCAAGTGTAAACTGTCTGACGTTCAAGACCTGTGCGTAATGG

AspValLeuLysGluValLysAlaAlaAlaSerLysValLysAlaAsnLeuLeuSerVal  
5581 AGGACGTACTCAAGGAGGTTAAAGCAGCGGCGTCAAAAGTGAAGGCTAACTTGCTATCCG  
TCCTGCATGAGTTCTCCAATTCGTCGCCGAGTTTTCACTTCCGATTGAACGATAGGC

GluGluAlaCysSerLeuThrProProHisSerAlaLysSerLysPheGlyTyrGlyAla  
5641 TAGAGGAAGCTTGAGCCTGACGCCCCACACTCAGCCAAATCCAAGTTTGGTTATGGGG  
ATCTCCTTCGAACGTCGGAAGTGCAGGGGGTGTGAGTGGTTAGGTTCAAACCAATACCCC

LysAspValArgCysHisAlaArgLysAlaValThrHisIleAsnSerValTrpLysAsp  
5701 CAAAAGACGTCCGTTGCCATGCCAGAAAGGCCGTAACCCACATCAACTCCGTGTGGAAAG  
GTTTTCTGCAGGCAACGGTACGGTCTTTCGGCATTGGGTGTAGTTGAGGCACACCTTTC

LeuLeuGluAspAsnValThrProIleAspThrThrIleMetAlaLysAsnGluValPhe  
5761 ACCTTCTGGAAGACAATGTAAACCAATAGACACTACCATCATGGCTAAGAACGAGGTTT  
TGGAAGACCTTCTGTTACATTGTGGTTATCTGTGATGGTAGTACCGATTCTTGCTCCAAA



# FIG. 32G

5821 CysValGlnProGluLysGlyGlyArgLysProAlaArgLeuIleValPheProAspLeu  
TCTGCGTTTCAGCCTGAGAAAGGGGGGTCGTAAGCCAGCTCGTCTCATCGTGTTCCTCCCGATC  
AGACGCAAGTCGGAAGTCTTCCCCCAGCATTGGTTCGAGCAGAGTAGCAAGGGGGCTAG

5881 GlyValArgValCysGluLysMetAlaLeuTyrAspValValThrLysLeuProLeuAla  
TGGGCGTGCCTGTGCGAAAAGATGGCTTTGTACGACGTGGTTACAAAGCTCCCTTGG  
ACCCGACGCGCACACGCTTTTCTACCGAAACATGCTGCACCAATGTTTCGAGGGGAACC

5941 ValMetGlySerSerTyrGlyPheGlnTyrSerProGlyGlnArgValGluPheLeuVal  
CCGTGATGGGAAGCTCCTACGGATTCCAATACTACCAAGGACAGCGGGTTGAATTCCTCG  
GGCACTACCTTCGAGGATGCCTAAGGTTATGAGTGGTCTGTGCGCCAACTTAAGGAGC

6001 GlnAlaTrpLysSerLysLysThrProMetGlyPheSerTyrAspThrArgCysPheAsp  
TGCAAGCGTGGAAAGTCCAAGAAAACCCCAATGGGGTTCTCGTATGATACCCGCTGCTTTG  
ACGTTTCGACCTTCAGGTTCTTTTGGGGTTACCCCAAGAGCATACTATGGGCGACGAAAC

6061 SerThrValThrGluSerAspIleArgThrGluGluAlaIleTyrGlnCysCysAspLeu  
ACTCCACAGTCACTGAGAGCGACATCCGTACGGAGGAGGCAATCTACCAATGTTGTGACC  
TGAGGTGTCAGTGACTCTCGCTGTAGGCATGCCTCCTCCGTTAGATGGTTACAACACTGG

6121 AspProGlnAlaArgValAlaIleLysSerLueThrGluArgLeuTyrValGlyGlyPro  
TCGACCCCAAGCCCGCTGGCCATCAAGTCCCTCACCGAGAGGCTTTATGTTGGGGGGC  
AGCTGGGGGTTTCGGGCGACCGGTAGTTACGGAGTGGCTCTCCGAAATACAACCCCGG

6181 LeuThrAsnSerArgGlyGluAsnCysGlyTyrArgArgCysArgAlaSerGlyValLeu  
CTCTTACCAATTCAAGGGGGGAGAACTGCGGCTATCGCAGGTGCGGCGGAGCGGCGTAC  
GAGAATGGTTAAGTTCCCCCTCTTGACGCCGATAGCGTCCACGGCGGCTCGCGCATG

6241 ThrThrSerCysGlyAsnThrLeuThrCysTyrIleLysAlaArgAlaAlaCysArgAla  
TGACAACTAGCTGTGGTAACACCCTCACTTGCTACATCAAGGCCCGGGCAGCCTGTGCGAG  
ACTGTTGATCGACACCATTTGTGGGAGTGAACGATGTAGTTCCGGGCGGCTCGGACAGCTC

6301 AlaGlyLeuGlnAspCysThrMetLeuValCysGlyAspAspLeuValValIleCysGlu  
CCGCGAGGGCTCCAGGACTGCACCATGCTCGTGTGTGGCGACGACTTAGTCGTTATCTGTG  
GGCGTCCCGAGGTCCTGACGTGGTACGAGCACACCCGCTGCTGAATCAGCAATAGACAC

6361 SerAlaGlyValGlnGluAspAlaAlaSerLeuArgAlaPheThrGluAlaMetThrArg  
AAAGCGCGGGGGTCCAGGAGGACGCGGCGAGCCTGAGAGCCTTCACGGAGGCTATGACCA  
TTTCGCGCCCCCAGGTCTCTGCGCGCTCGGACTCTCGGAAGTGCTCCGATACTGGT

6421 TyrSerAlaProProGlyAspProProGlnProGluTyrAspLeuGluLeuIleThrSer  
GGTACTCCGCCCCCTGGGGACCCCAACAGAAATACGACTTGGAGCTCATAACAT  
CCATGAGGCGGGGGGACCCCTGGGGGGTGTGGTCTTATGCTGAACCTCGAGTATTGTA

6481 CysSerSerAsnValSerValAlaHisAspGlyAlaGlyLysArgValTyrTyrLeuThr  
CATGCTCCTCCAACGTGTCAAGTCGCCCACGACGGCGCTGGAAAGAGGGTCTACTACCTCA  
GTACGAGGAGGTTGCACAGTCAGCGGGTGTGCCGCGACCTTTCTCCAGATGATGGAGT

6541 ArgAspProThrThrProLeuAlaArgAlaAlaTrpGluThrAlaArgHisThrProVal  
CCCGTGACCTTACAACCCCTCGCGAGAGCTGCGTGGGAGACAGCAAGACACACTCCAG  
GGCACTGGGATGTTGGGGGGAGCGCTCTCGACGCACCTCTGTGCTGTGTGAGGTC

6601 AsnSerTrpLeuGlyAsnIleIleMetPheAlaProThrLeuTrpAlaArgMetIleLeu  
TCAATTCCTGGCTAGGCAACATAATCATGTTTGGCCCCACACTGTGGGCGAGGATGATAC  
AGTTAAGGACCGATCCGTTGTATTAGTACAAACGGGGGTGTGACACCCGCTCCTACTATG

6661 MetThrHisPhePheSerValLeuIleAlaArgAspGlnLeuGluGlnAlaLeuAspCys  
TGATGACCCATTCTTTAGCGTCTTATAGCCAGGGACAGCTTGAACAGGCCCTCGATT  
ACTACTGGGTAAAGAAATCGCAGGAATATCGGTCCTGCTGCAACTGTCCGGGAGCTAA

6721 GluIleTyrGlyAlaCysTyrSerIleGluProLeuAspLeuProProIleIleGlnArg  
GCGAGATCTACGGGGCCTGCTACTCCATAGAACCCTTGATCTACCTCCAATCATTCAA  
CGCTCTAGATGCCCCGACGATGAGGTATCTTGGTGAACCTAGATGGAGGTTAGTAAGTTT

6781 Leu  
GACTC  
CTGAG



FIG. 33

Lane Number	Chimp Reference Number	Infection Type	Sample date (days) (0=inoculation day)	ALT (alanine) aminotransferase level in sera (μU/ml)
1	1	NANB	0	0
2	1	NANB	76	71
3	1	NANB	118	19
4	1	NANB	154	N/A
5	2	NANB	0	0
6	2	NANB	21	52
7	2	NANB	73	13
8	2	NANB	138	N/A
9	3	NANB	0	8
10	3	NANB	43	205
11	3	NANB	53	14
12	3	NANB	159	6
13	4	NANB	-3	11
14	4	NANB	55	132
15	4	NANB	83	N/A
16	4	NANB	140	N/A
17	5	HAV	0	4
18	5	HAV	25	147
19	5	HAV	40	18
20	5	HAV	268	5
21	6	HAV	-8	N/A
22	6	HAV	15	100
23	6	HAV	41	10
24	6	HAV	129	N/A
26	7	HAV	0	7
27	7	HAV	22	83
28	7	HAV	115	5
29	7	HAV	139	N/A
30	8	HAV	0	15
31	8	HAV	26	130
32	8	HAV	74	8
33	8	HAV	205	5
34	9	HBV	-290	N/A
35	9	HBV	379	9
36	9	HBV	435	6
37	10	HBV	0	8
38	10	HBV	111-118 (pool)	96-156 (pool)
39	10	HBV	205	9
40	10	HBV	240	13
41	11	HBV	0	11
42	11	HBV	28-56 (pool)	8-100 (pool)
43	11	HBV	169	9
44	11	HBV	223	10

FIG. 33A

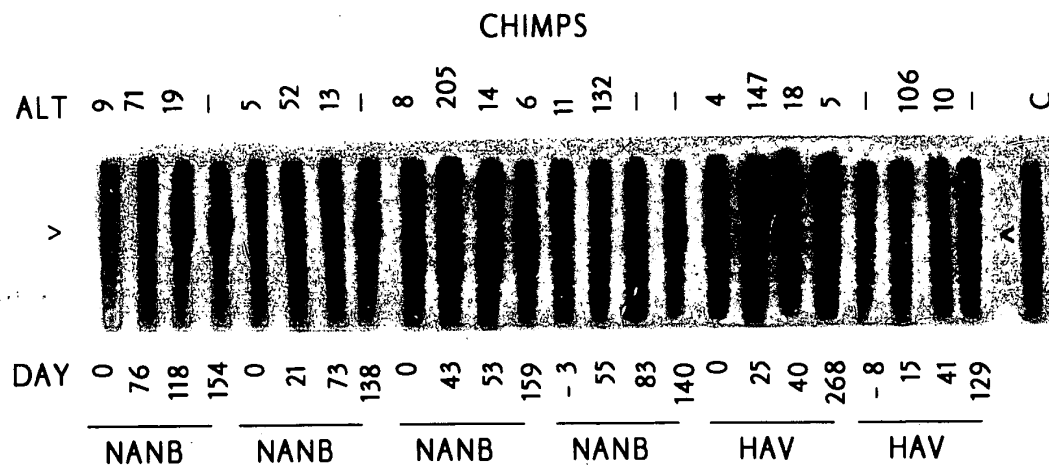


FIG. 33B

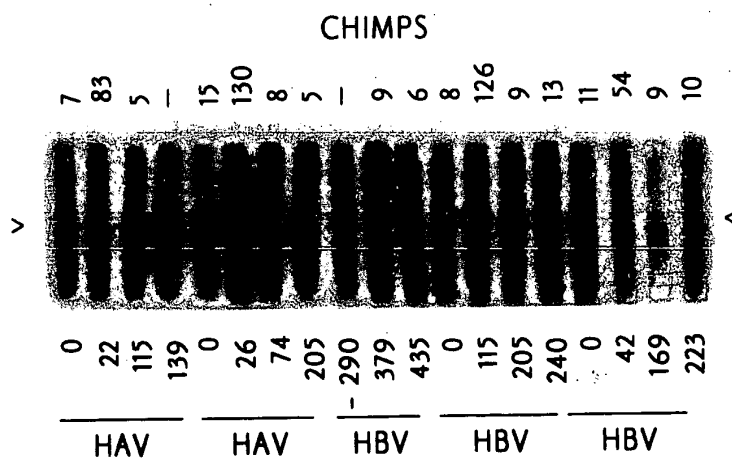




FIG. 34

Lane Number	Patient Reference Number	Diagnosis	ALT Level ( $\mu\text{u/ml}$ )
1	1 <sup>1</sup>	NANB	1354
2	1 <sup>1</sup>	NANB	31
3	2 <sup>1</sup>	NANB	14
4	2 <sup>1</sup>	NANB	79
5	2 <sup>1</sup>	NANB	26
6	3 <sup>1</sup>	NANB	78
7	3 <sup>1</sup>	NANB	87
8	3 <sup>1</sup>	NANB	25
9	4 <sup>1</sup>	NANB	60
10	4 <sup>1</sup>	NANB	13
11	5 <sup>1</sup>	NANB	298
12	5 <sup>1</sup>	NANB	101
13	6 <sup>1</sup>	NANB	474
14	6 <sup>1</sup>	NANB	318
15	7 <sup>1</sup>	NANB	20
16	7 <sup>1</sup>	NANB	163
17	8 <sup>1</sup>	NANB	44
18	8 <sup>1</sup>	NANB	50
19	9	NANB	N/A
20	10	NANB	N/A
21	11	NANB	N/A
22	12	Normal	N/A
23	13	Normal	N/A
24	14	Normal	N/A
26	30174	Normal	N/A
27	30105	Normal	N/A
28	30072	Normal	N/A
29	30026	Normal	N/A
30	30146	Normal	N/A
31	30250	Normal	N/A
32	30071	Normal	N/A
33	15	AcuteHAV	N/A
34	16	AcuteHAV	N/A
35	17	AcuteHAV	N/A
36	18	AcuteHAV	N/A
37	48088	AcuteHAV	N/A
38	47288	AcuteHAV	N/A
39	47050	AcuteHAV	N/A
40	46997	AcuteHAV	N/A
41	19	Convalescent HBV	N/A
42	20	(anti-HBSag+ve;	N/A
43	21	anti-HBCag+ve)	N/A
44	22	(anti-HBSag+ve;	N/A
45	23	anti-HBCag+ve)	N/A
46	24	(anti-HBSag+ve;	N/A
47	25	anti-HBCag+ve)	N/A
48	26	(anti-HBSag+ve;	N/A
49	27	anti-HBSag+ve)	N/A

<sup>1</sup>Sequential serum samples were assayed from these patients



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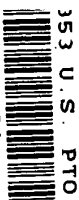


FIG. 34A

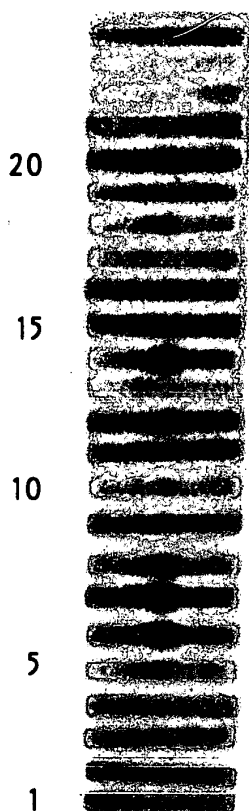


FIG. 34B

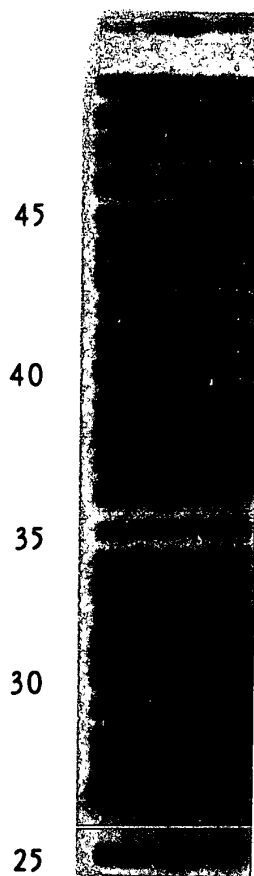
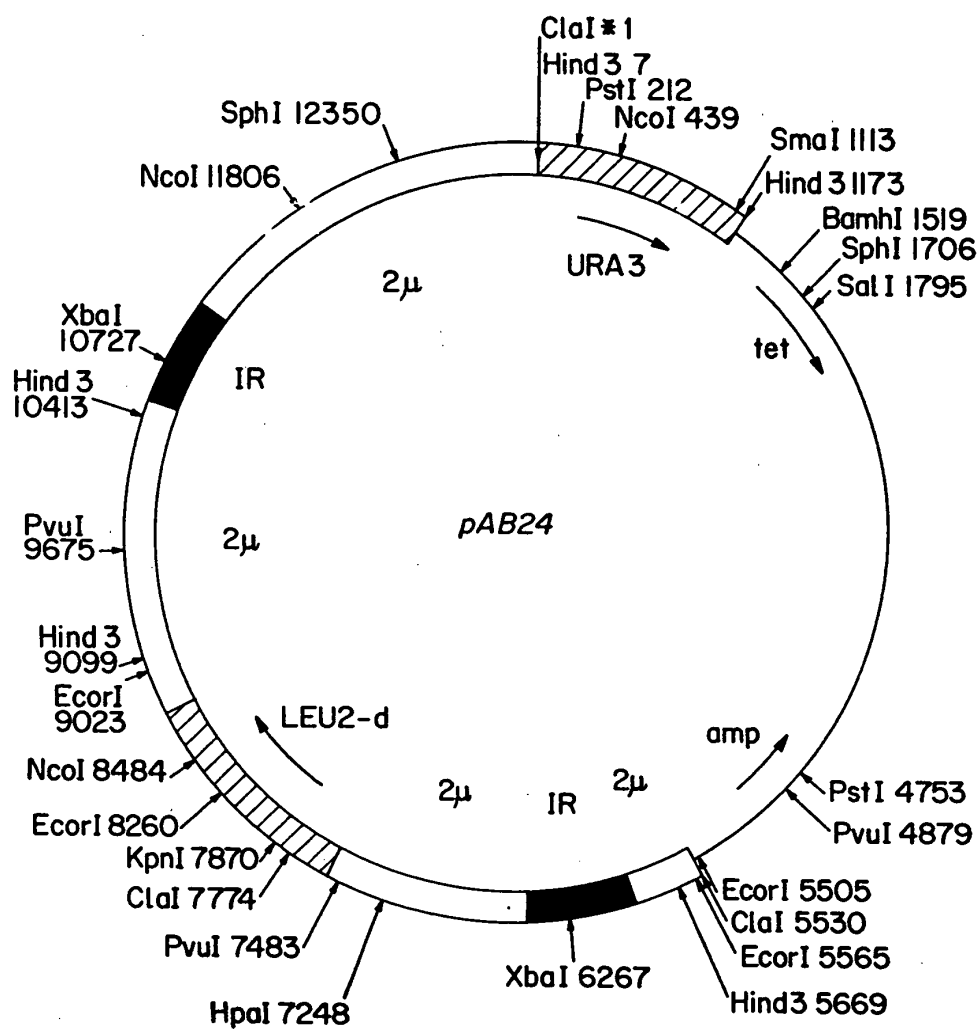




FIG. 35



**FIG. 36A**

[illegible]



01/27/03  
:853 U.S. PTO

FIG. 37A

1 2 3

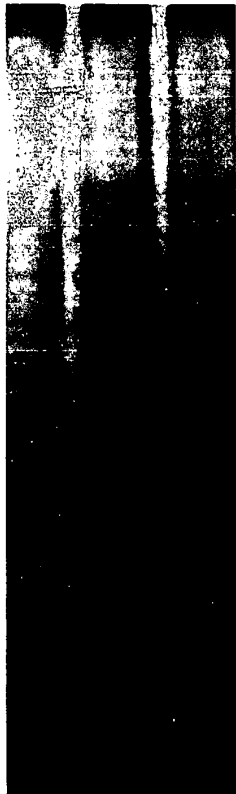


FIG. 37B

1 2

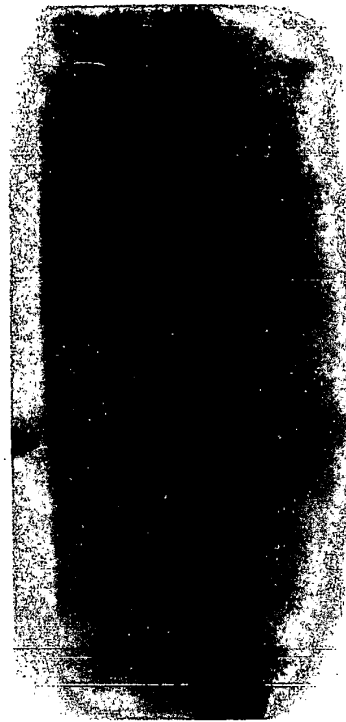


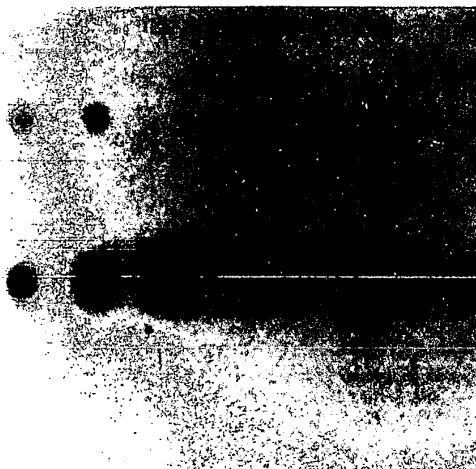
FIG. 38

1 2 3 4



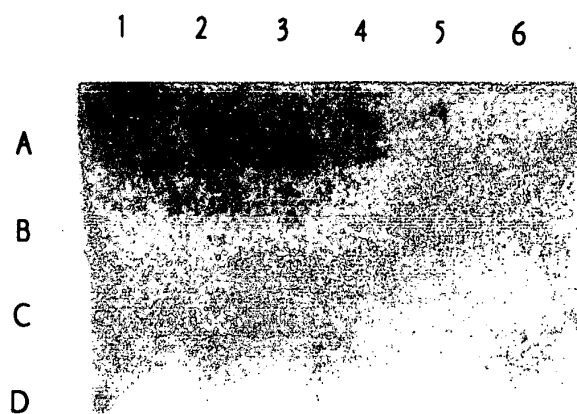
FIG. 40

1 2 3 4



3 U.S. PTO  
1/27/03

FIG. 39



01/27/03  
C853 U.S. PTO

FIG. 41A

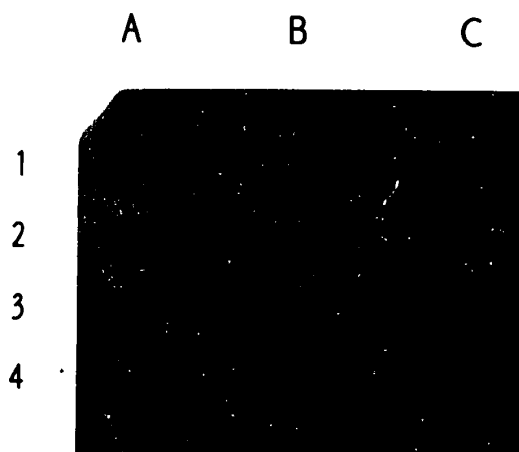
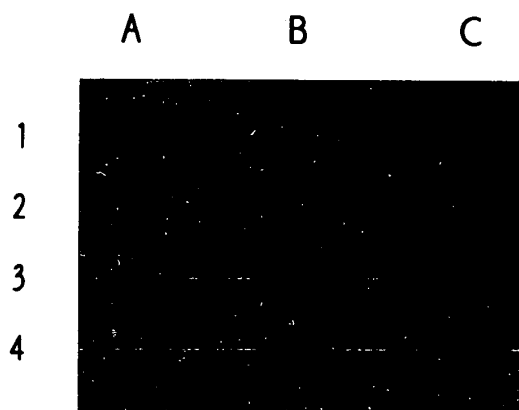


FIG. 41B





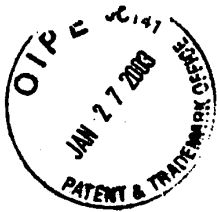


FIG. 42A

HCV	10	20	30	40	50
	EYVLLFLL	LADARVCS	LWMMLISQ	AEALNLVIL	NAASLAGTHGLV
MNWVD1	130	140	150	160	170
	AVSFVTLITGN	MSFRDLGR	VMVMGATMT	DDIGMGVTYL	ALLAAFKVRPT
	180				
HCV	60	70	80	90	100
	WYLGKGWPG	AVYTFYGM	WPLLLLLL	ALPQRAYALD	TEVAASCGGV
MNWVD1	190	200	210	220	230
	TSKELMMTTI	GIVLLSQST	IPETILELTD	ALALGMMVL	KMVRKMEKYQ
	240				
HCV	120	130	140	150	160
	KRYISWCLW	LQYFLTRV	EAQLHVWIP	PLNVRGGRDA	VILLMCAVHPT
MNWVD1	250	260	270	280	290
	NAVILQNAWK	VSCITILAV	VSVSPLFLT	SSQQKADWIP	LALTIKGLNPT
HCV	180	190	200	210	220
	FGPLWILQAS	LLKVPYF-V	RVQGLLRF-C	ALARKMIGGH	YVQMVIKLGAL
MNWVD1	300	310	320	330	340
	KKRSWPLNEA	IMAVGMVSI	LASSLLKNDI	PMTGPLVAGG	LLTVCYV-LTGR
HCV	240	250	260	270	280
	TPLRDWAHNG	LRDLAVAVE	PVVFSSQMET	KLITWGADTA	ACGDIINGLPV
MNWVD1	360	370	380	390	400
	ADV-K-WEDQ	AEISGSSPIL	SITISE-DGSM	SIKNEEEEQTL	ILIRTGLLVISG
HCV	300	310	320	330	340
	PADGMVSKGW	RLLAPITAYA	QQTRGLLGCI	ITSLTGRDKN	QVEGEVQIVSTA
MNWVD1	420	430	440	450	460
	VSIPITAAAW	YLWEVKQRAG	VLWDVPSPP	PVGKAELEDG	AYRIKQKGLGYS
HCV	360	370	380	390	400
	INGVCWTVYH	GAGTRTIAS	PKGPVIQMYT	NVDQDLV----	GWPAPQGSRLT
MNWVD1	480	490	500	510	520
	KEGTFTMWH	VTRGAVLMH	KGKRIPSWAD	VKKDLVSCGGG	WKLEGEWKEGE
HCV	420	430	440	450	460
	LYLVTRHAD	VIPVRRRGDS	RGSLLSPRPIS	YKLGSSGGPLL	CPAGHAVGIFRA
MNWVD1	540	550	560	570	580
	PGKNPRAVQT	KPGLFKTN--	AGTIGAVSLD	FSPGTSGSPII	DKKGKVVLGYG

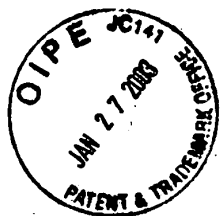


FIG. 42B

HCV           480           490           500           510           520           530  
AKAVDFIPVENLETTMRSPVFTDNSSPPVVPQSFQVAHLHAPTGSQKS--TKVPAAYAAQ  
MNWVD1    AYVSAIAQTEK--SIEDNPEIEDDIFRK---RKLTIMDLHPGAGKTKRYLPAIVRGAIKR  
                 600           610           620           630           640

HCV           540           550           560           570           580  
GYKVLVLNPS--VAATLGFGAYMSKAHGIDPNIRTGVRTITTGSPITYSTYGGKFLADGGC  
MNWVD1    GLRTLILAPTRVVAAEMEEALRGLPIRYQTPAIRAEHTGREIVDLMCHATFTMRLL-SPV  
                 650           660           670           680           690           700

HCV           590           600           610           620           630           640  
SGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV  
MNWVD1    RVPNYNLIIMDEAHFTDPAIAARGYISTRVE-MGEAAGIFMTATPPGSRD-PFPQSNAP  
                 710           720           730           740           750           760

HCV           650           660           670           680           690           700  
ALSTTGEIPFYGKAIPLEVIKGGRRHLIFCHSKKKCELA AAKLVALGINAVAYYRGLDVSV  
MNWVD1    IMDEEREIPERSWSSGHEWVTD FKGKT VWFVPSIKAGNDTAACL RKGK KVTQLSRKTFD  
                 770           780           790           800           810           820

HCV           710           720           730           740           750           760  
IPTSGDVVVVATDALMTGYTGDFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSRT  
MNWVD1    SEYVKTRTNDWNFVTTDISEMGANFKAERVIDPRRCMKPVILTDGEERVILAGPMPVTH  
                 830           840           850           860           870           880

HCV           770           780           790           800           810           820  
QRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT  
MNWVD1    SS

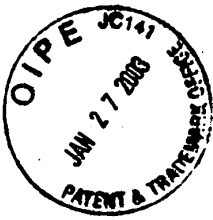


FIG. 43

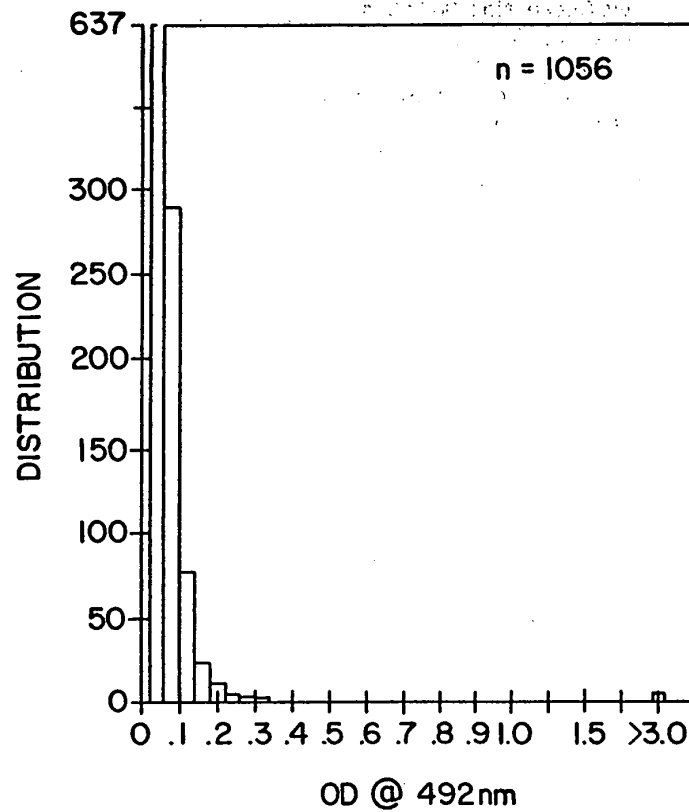
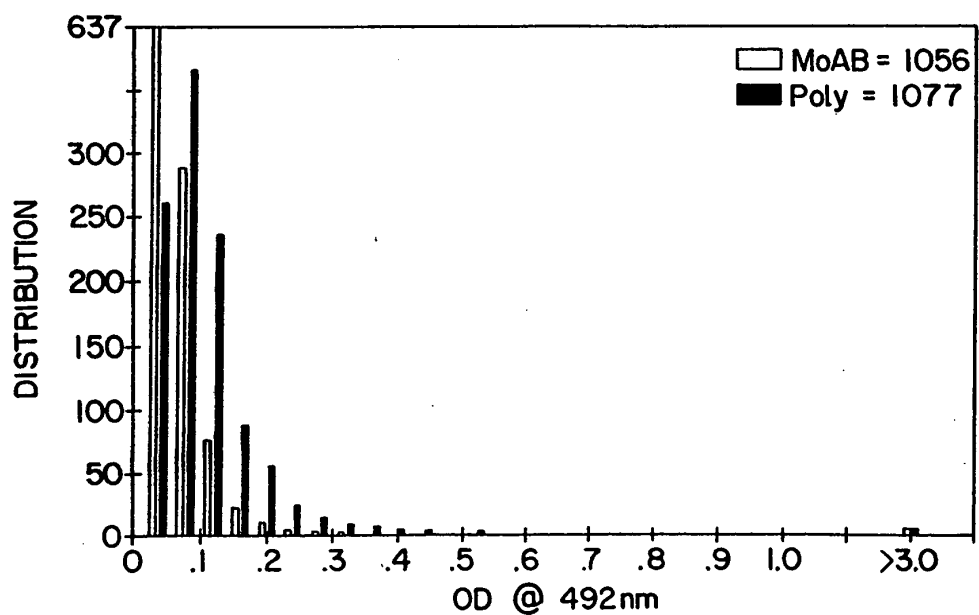


FIG. 44



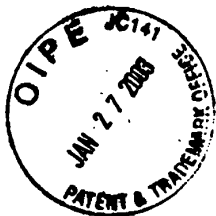


FIG. 45

<u>Name</u>	<u>Common Sequence</u>	<u>Variable Sequence</u>
5'-3-1	AAGCTTGATCGAATTC	CGATCTTGC
-2		CGATCCTGC
-3		CGATCATGC
-4		CGATCGTGC
-5		CGAAGTTGC
-6		CGAAGCTGC
-7		AGATCTTGC
-8		AGATCCTGC
-9		AGATCATGC
-10		AGATCGTGC
-11		AGAAGTTGC
-12		AGAAGCTGC
-13		CGATCTTGT
-14		CGATCCTGT
-15		CGATCATGT
-16		CGATCGTGT
-17		CGAAGTTGT
-18		CGAAGCTGT
-19		AGATCTTGT
-20		AGATCCTGT
-21		AGATCATGT
-22		AGATCGTGT
-23		AGAAGTTGT
-24		AGAAGCTGT
-25		CGCTCTTGC
-26		CGCTCCTGC
-27		CGCTCATGC
-28		CGCTCGTGC
-29		CGCAGTTGC
-30		CGCAGCTGC
-31		CGCTCTTGT
-32		CGCTCCTGT
-33		CGCTCATGT
-34		CGCTCGTGT
-35		CGCAGTTGT
-36		CGCAGCTGT



FIG. 46A

GlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGlyTrpGly  
1 CAGGCTGTCCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTGTGACCAGGGCTGGG  
GTCCGACAGGACTCTCCGATCGGTCGACGGCTGGGAATGGCTAAACTGGTCCCCGACCC

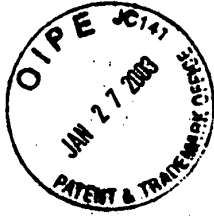
ProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHisTyrPro  
61 GCCCTATCAGTTATGCCAACGGAACGGCCCCCGACCAAGCCCCCTACTGTGGCACTACC  
CGGATAGTCAATACGGTTGCCCTTCGCCGGGGCTGTCGCGGGGATGACGACCGTGATGG

ProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCysPheThr  
121 CCCCAAAACCTTGCGGTATTGTGCCCGCGAAGAGTGTGTGTCGGTCCGGTATATTGCTTCA  
GGGGTTTGGAAACGCCATAACACGGGCGCTTCTCACACACACACAGGCCCATATAACGAAGT

ProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSerTrpGly  
181 CTCCCAGCCCCGTGGTGGTGGAAACGACCAAGTCCGGCGCGCCACCTACAGCTGGG  
GAGGTCGGGGCACCAACCCCTTGCTGGCTGTCCAGCCCCCGCGGGTGGATGTCGACCC

GluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsnTrpPhe  
241 GTGAAAATGATACGGACGCTCTCGTCCTTAACAATACCAGGCCACCGCTGGGCAATTGGT  
CACTTTTACTATGCCCTGCAGAACGAGGAATTGTTATGTCGCGTGGCAGCCCCGTTAACCA

GlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProProCysVal  
301 TCGGTTGTACCTGGATGAACCTCAACTGGATTCAACCAAGTGTGCGGAGCGCCTCCTTGTG  
AGCCAAACATGGACCTACTTGAGTTGACCTAAGTGGTTTCACACGCGCTCGCGGAGGAACAC



## FIG. 46B

IleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLysHisPro  
361 TCATCGGAGGGGGCAACAACACCCCTGCACCTGCCACTGCTTCCGCAAGCATC  
AGTAGCCCTCCCCCGTTGTGTGGACGTGACGGGTGACTAACGAAGGCTTCGTAG

AspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeuValAsp  
421 CGGACGCCACATACTCTCGGTGCGCTCCGGTCCCTGGATCACACCCAGGTGCCTGTCG  
GCCTGCGGTGTATGAGAGCCACGCCGAGGCCAGGACCTAGTGTGGTCCACGGACGAGC

-----  
TyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLysIleArg  
481 ACTACCCGTATAGGCTTTGGCATTATCCTTGTACCATCAACTACTATATTTAAATCA  
TGATGGGCATATCCGAAACCGTAATAGGAACATGGTAGTTGATGATATAAATTTTAGT

-----  
MetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArgGlyGlu  
541 GGATGTACGTGGAGGGGTCCGAGCACAGGCTGGAAAGTGCCTGCACACTGGACGCGGGCG  
CCTACATGCACCCCTCCCCAGCTCGTGTCCGACCTTCGACGGACGTTGACCTGCGCCCCCGC

-----  
ArgCysAspLeuGluAspArgAspArgSerGluLeuSerProLeuLeuThrThrThr  
601 AACGTTGCGATCTGGAAGATAGGACAGGTCCGAGCTCAGCCCCGTTACTGCTGACCCACTA  
TTGCAACGCTAGACCTTCTATCCCTGTCCAGGCTCGAGTCGGGCAATGACGACTGGTGAT

-----  
GlnTrpGlnValLeuProCysSerPheThrThrLeuProAlaLeuSerThrGlyLeuIle  
661 CACAGTGGCAGGTCTCCCGTGTTCCTTCAAAACCCCTGCCAGCCTTGTCCACCGGCTCA  
GTGTCAACCGTCCAGGAGGGCACAAAGGAAGTGTGGGACGGTCCGGAACAGGTGGCCGGAGT



FIG. 46C

-----Overlap with Combined ORF of DNAs 12f through 15e-----  
HisLeuHisGlnAsnIleValAspValGlnTyrLeuTyrGlyValGlySerSerIleAla  
721 TCCACCTCCACCAGAACATTGTGGACGTGCAGTACTTGTACGGGTGGGTCAAGCATCG  
AGGTGGAGGTGGTCTTGTAAACACCTGCACGTCATGAACATGCCCCACCCAGTTCGTAGC  
-----  
SerTrpAlaIleLysTrpGluTyrValValLeuLeuPheLeuLeuAlaAspAlaArg  
781 CGTCTGGGCCATTAAAGTGGAGTACGTCCTCCTGTTCTTCTGCTTGCAGACGCGC  
GCAGGACCCGGTAATTCAACCTCATGCAGCAGGAGACAAGGAAGACGAACGTCTGCGCG  
-----  
ValCysSerCysLeuTrpMetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsn  
841 GCGTCTGCTCCTGCTGTGGATGATGCTACTCATATCCCAAGCGGAAGCGGCTTTGGGAGA  
CGCAGACGAGGACGAACACCTACTACGATGAGTATAGGTTGCGCTTCCGCCGAAACCTCT  
-----  
LeuValIleLeuAsnAlaAlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuVal  
901 ACCTCGTAATACTTAATGCAGCATCCCTGGCCGGACGCACGGTCTTGTATCCTTCCTCG  
TGGAGCATTATGAATTACGTCGTAGGGACCGGCCCTGCGTGCAGAACATAGGAAGGAGC  
-----  
PhePheCysPheAlaTrpTyrLeuLysGlyLysTrpValProGlyAlaValTyrThrPhe  
961 TGTTCCTTCTGCTTTCATGGTATCTGAAGGGTAAGTGGTGCCCCGAGCGGTCTACACCT  
ACAAGAGACGAAACGTACCATAGACTTCCCATTCACCCACGGGCTCGCCAGATGTGGA



FIG. 46D

-----  
TyrGlyMetTrpProLeuLeuLeuLeuAlaLeuProGlnArgAlaTyrAlaLeu  
1021 TCTACGGGATGTGGCCTCTCCTCCTGCTGCTGGCGTTGCCCGGCGTACGCGC  
AGATGCCCTACACCGGAGAGGAGGACGAGACAACCGCAACGGGTGCGCCGCAATGCGCG

-----  
AspThrGluValAlaAlaSerCysGlyGlyValValLeuValGlyLeuMetAlaLeuThr  
1081 TGGACACGGAGTGGCGCGTCTGCTGGCGGTGTGTTCTCTCGTCGGGTGATGGCGCTAA  
ACCTGTGCTCCACCGGCGCAGCACACCGCCACAACAAGACGAGCCCCAACTACCGCGATT

-----  
LeuSerProTyrTyrLysArgTyrIleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeu  
1141 CTCTGTCAACCATATTACAAGCGCTATATCAGCTGGTGTGTTGTGGCTTCAATATTTC  
GAGACAGTGGTATAATGTTCGCGGATATAGTCGACCACGAACACCCGGAAGTCATAAAAG

-----  
ThrArgValGluAlaGlnLeuHisValTrpIleProProLeuAsnValArgGlyGlyArg  
1201 TGACCAGAGTGAAGCGCAACTGCACGTGTGGATTCCCCCTCAACGTCCGAGGGGGC  
ACTGGTCTCACCTTCGCGTTGACGTGCACACCTAAGGGGGGAGTTGCAGGCTCCCCCGC

-----  
AspAlaValIleLeuLeuMetCysAlaValHisProThrLeuValPheAspIleThrLys  
1261 GCGACGCTGTCACTTACTCATGTGTGTGTACACCGACTCTGGTATTTGACATCACCA  
CGCTGCGACAGTAGAATGAGTACACACGACATGTGGGCTGAGACCATAAACTGTAGTGGT

-----  
LeuLeuLeuAlaValPheGlyProLeuTrpIleLeuGlnAla  
1321 AATTGCTGTGGCGTCTTCGGACCCCTTGGATTCTTCAAGCCAG  
TTAACGACGACCGGCAGAGCCTGGGGAAACCTAAGAAGTTCCGGTC





FIG. 47A

1 GlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGlyTrpGly  
CAGGCTGTCCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACCAGGGCTGGG  
GTCCGACAGGACTCTCCGATCGGTCGACGGCTGGGGAATGGCTAAACTGGTCCCGACCC

61 ProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHisTyrPro  
GCCCTATCAGTTATGCCAACGGAAGCGGCCCGACCGAGCGCCCTACTGCTGGCACTACC  
CGGGATAGTCAATACGGTTGCCCTCGCCGGGGCTGGTCGCGGGGATGACGACCGTGATGG

121 ProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCysPheThr  
CCCCAAACCTTGCGGTATTGTGCCCGCGAAGAGTGTGTGGTCCGGTATATTGCTTCA  
GGGGTTTTGGAACGCCATAACAGGGCGCTTCTCACACACACAGGCCATATAACGAAGT

181 ProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSerTrpGly  
CTCCAGCCCCGTGGTGGTGGGAACGACCGACAGGTGCGGCGCGCCACCTACAGCTGGG  
GAGGGTCGGGGCACCACCACCTTGTGCTGTCCAGCCGCGCGGGTGATGTCGACCC

241 GluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsnTrpPhe  
GTGAAAATGATACGGACGTCTTCGTCTTAACAATACAGGCCACCGCTGGGCAATTGGT  
CACTTTTACTATGCCTGCAGAACGAGGAATTGTTATGGTCCGGTGGCGACCCGTTAACCA

301 GlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProProCysVal  
TCGGTTGTACCTGGATGAACCTCAACTGGATTACCAAAGTGTGCGGAGCGCTCCTTGTG  
AGCCAACATGGACCTACTTGAGTTGACCTAAGTGGTTTACACGCCTCGCGGAGGAACAC

361 IleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLysHisPro  
TCATCGGAGGGGCGGGCAACAACACCCTGCACTGCCCCACTGATTGCTTCGCAAGCATC  
AGTAGCTCCCCGCGCGTTGTGTGGGACGTGACGGGGTGACTAACGAAGGCGTTCGTAG

421 AspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeuValAsp  
CGGACGCCACATACTCTCGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTGCCTGGTCG  
GCCTGCGGTGTATGAGAGCCACGCCGAGGCCAGGGACCTAGTGTGGGTCCACGGACAGC

481 TyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLysIleArg  
ACTACCGTATAGGCTTTGGCATTATCCTTGTACCATCACTACACCATATTTAAATCA  
TGATGGGCATATCCGAAACCGTAATAGGAACATGGTAGTTGATGTGGTATAAATTTAGT

541 MetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArgGlyGlu  
GGATGTACGTGGGAGGGGTCGAACACAGGCTGGAAGCTGCCTGCAACTGGACGCGGGGCG  
CCTACATGCACCCTCCCCAGCTTGTGTCCGACCTTCGACGGACGTTGACCTGCGCCCCGC

601 ArgCysAspLeuGluAspArgAspArgSerGluLeuSerProLeuLeuLeuThrThrThr  
AACGTTGCGATCTGGAAGACAGGGACAGGTCCGAGCTCAGCCCGTTACTGCTGACCACTA  
TTGCAACGCTAGACCTTCTGTCCCTGTCCAGGCTCGAGTCGGGCAATGACGACTGGTGAT

661 GlnTrpGlnValLeuProCysSerPheThrThrLeuProAlaLeuSerThrGlyLeuIle  
CACAGTGGCAGGTCTCCCGTGTCTTCCACCAACCCTACCAGCCTGTCCACCGGCCTCA  
GTGTCACCGTCCAGGAGGGCACAAGGAAGTGTGGGATGGTCGGAACAGGTGGCCGGAGT

721 HisLeuHisGlnAsnIleValAspValGlnTyrLeuTyrGlyValGlySerSerIleAla  
TCCACCTCCACCAGAACATTGTGGACGTGCAGTACTTGTACGGGGTGGGGTCAAGCATCG  
AGGTGGAGGTGGTCTTGTAAACACCTGCACGTCATGAACATGCCCCACCCAGTTCGTAGC

781 SerTrpAlaIleLysTrpGluTyrValValLeuLeuPheLeuLeuAlaAspAlaArg  
CGTCCTGGGCCATTAAGTGGGAGTACGTGCTTCTCCTGTTCTTCTGCTTGACAGACGCGC  
GCAGGACCCGGTAATTCACCTCATGCAGCAAGAGGACAAGGAAGACGAACGTCTGCGCG

841 ValCysSerCysLeuTrpMetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsn  
GCGTCTGCTCCTGCTTGTGGATGATGCTACTCATATCCCAAGCGGAGGCGCTTTGGAGA  
CGCAGACGAGGACGAACACCTACTACGATGAGTATAGGGTTCGCTCCGCCGAAACCTCT

901 LeuValIleLeuAsnAlaAlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuVal  
ACCTCGTAATACTTAATGCAGCATCCCTGGCCGGGACGCACGGTCTTGATCCTTCCTCG  
TGGAGCATTATGAATTACGTCGTAGGGACCGCCCTGCGTGCCAGAACATAGGAAGGAGC



# FIG. 47B

PhePheCysPheAlaTrpTyrLeuLysGlyLysTrpValProGlyAlaValTyrIhrPhe  
961 TGTTCCTTCTGCTTTGCATGGTATTTGAAGGGTAAGTGGGTGCCCGAGCGGTCTACACCT  
ACAAGAAGACGAAACGTACCATAAACTTCCCATTACCCACGGGCTCGCCAGATGTGGA

TyrGlyMetTrpProLeuLeuLeuLeuLeuAlaLeuProGlnArgAlaTyrAlaLeu  
1021 TCTACGGGATGTGGCCTCTCCTCCTGCTCCTGTTGGCGTTGCCCAAGCGGGCTACGCGC  
AGATGCCCTACACGGAGAGGAGGACGAGGACAACCGCAACGGGGTGCCTCGCATGCGCG

AspThrGluValAlaAlaSerCysGlyGlyValValLeuValGlyLeuMetAlaLeuThr  
1081 TGGACACGGAGGTGGCGCGTCGTGTGGCGGTGTTGTCTCGTCGGGTTGATGGCGCTGA  
ACCTGTGCCTCCACCGGCGCAGCACACCGCCACAACAAGAGCAGCCAACTACCGCGACT

LeuSerProTyrTyrLysArgTyrIleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeu  
1141 CTCTGTCAACATATTACAAGCGCTATATCAGCTGGTGCTTGTGGTGGCTTCACTATTTTC  
GAGACAGTGGTATAATGTTCCGATATAGTCGACCACGAACACCGAAGTCATAAAAG

ThrArgValGluAlaGlnLeuHisValTrpIleProProLeuAsnValArgGlyGlyArg  
1201 TGACCAGAGTGGAAAGCGCAACTGCACGTGTGGATTCCCCCTCAACGTCGAGGGGGC  
ACTGGTCTCACCTTCGCGTTGACGTGCACACCTAAGGGGGGAGTTGCAGGCTCCCCCG

AspAlaValIleLeuLeuMetCysAlaValHisProThrLeuValPheAspIleThrLys  
1261 GCGACGCGCTCATCTTACTCATGTGTGCTGTACACCGACTCTGGTATTTGACATCACCA  
CGCTGCGGCAGTAGAATGAGTACACACGACATGTGGGCTGAGACCATAAACTGTAGTGGT

LeuLeuLeuAlaValPheGlyProLeuTrpIleLeuGlnAlaSerLeuLeuLysValPro  
1321 AATTGCTGCTGGCGCTCTTCGGACCCCTTTGGATTCTTCAAGCCAGTTTGCTTAAAGTAC  
TTAACGACGACCGGCAGAAAGCCTGGGAAACCTAAGAAGTTCGGTCAAACGAATTTTCATG

TyrPheValArgValGlnGlyLeuLeuArgPheCysAlaLeuAlaArgLysMetIleGly  
1381 CCTACTTTGTGCGCGTCCAAGGCCTTCTCCGGTTCTGCGGTTAGCGCGGAAGATGATCG  
GGATGAAACACGCGCAGGTTCCGGAAGAGGCCAAGACGCGCAATCGCGCTTCTACTAGC

GlyHisTyrValGlnMetValIleIleLysLeuGlyAlaLeuThrGlyThrTyrValTyr  
1441 GAGGCCATTACGTGCAAAATGGTCATCATTAAAGTTAGGGGCGCTTACTGGCACCTATGTTT  
CTCCGGTAATGCACGTTTACAGTAGTAATTCAATCCCCGCAATGACCGTGGATACAAA

AsnHisLeuThrProLeuArgAspTrpAlaHisAsnGlyLeuArgAspLeuAlaValAla  
1501 ATAACCATCTCACTCCTCTTCGGGACTGGGCGCACACGGCTTGCAGATCTGGCCGTGG  
TATTGGTAGAGTGAGGAGAAGCCCTGACCCGCGTGTGCGCAACGCTTAGACCGGCACC

ValGluProValValPheSerGlnMetGluThrLysLeuIleThrTrpGlyAlaAspThr  
1561 CTGTAGAGCCAGTCGTCTTCTCCAAATGGAGACCAAGCTCATCACGTGGGGGGCAGATA  
GACATCTCGGTCAGCAGAAAGAGGTTTACCTCTGGTTCGAGTAGTGCACCCCCGCTAT

AlaAlaCysGlyAspIleIleAsnGlyLeuProValSerAlaArgArgGlyArgGluIle  
1621 CCGCCGCGTGGCGGTGACATCATCAACGGCTTGCTGTTTCCGCCGAGGGGGCGGAGA  
GGCGGCGCACGCCACTGTAGTAGTTGCCGAACGGACAAAGCGGGGCTCCCCGGCCCTCT

LeuLeuGlyProAlaAspGlyMetValSerLysGlyTrpArgLeuLeuAlaProIleThr  
1681 TACTGCTCGGGCCAGCCGATGGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCATCA  
ATGACGAGCCCGGTGCGCTACCTTACCAGAGGTTCCCACTCCAACGACCGCGGGTAGT

AlaTyrAlaGlnGlnThrArgGlyLeuLeuGlyCysIleIleThrSerLeuThrGlyArg  
1741 CGGCGTACGCCCAGCAGACAAGGGGCTCTAGGGTGCTAATACCAAGCCTAACTGGCC  
GCCGATGCGGGTCGTCTGTTCCCGGAGGATCCACGTATTAGTGGTGGATTGACCGG

AspLysAsnGlnValGluGlyGluValGlnIleValSerThrAlaAlaGlnThrPheLeu  
1801 GGGACAAAACCAAGTGGAGGGTGAGGTCCAGATTGTGTCAACTGCTGCCAAACCTTCC  
CCCTGTTTTTGGTTCACCTCCCACTCCAGGTCTAACACAGTTGACGACGGGTTTGGAAAG

AlaThrCysIleAsnGlyValCysTrpThrValTyrHisGlyAlaGlyThrArgThrIle  
1861 TGGCAACGTGCATCAATGGGGTGTGCTGGACTGTCTACCACGGGGCGGAACGAGGACCA  
ACCGTTGCACGTAGTTACCCACACGACCTGACAGATGGTGGCCCGGCTTGCTCTCTGGT

AlaSerProLysGlyProValIleGlnMetTyrThrAsnValAspGlnAspLeuValGly  
1921 TCGCGTCACCAAGGGTCTGTCTCATCCAGATGTATACCAATGTAGACCAAGACCTTGTGG

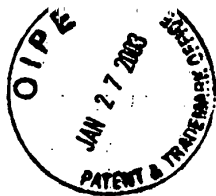


FIG. 47C

TrpProAlaProGlnGlySerArgSerLeuThrProCysThrCysGlySerSerAspLeu  
1981 GCTGGCCCCGCTCCGCAAGGTAGCCGCTCATTGACACCCTGCACTTGC GGCTCCTCGGACC  
CGACCGGGCGAGGCGTTCATCGGCGAGTAACTGTGGGACGTGAACGCCGAGGAGCCTGG

TyrLeuValThrArgHisAlaAspValIleProValArgArgArgGlyAspSerArgGly  
2041 TTTACCTGGTCACGAGGCGCCGATGTCTTCCGTGCGCGGGCGGGGTGATAGCAGGG  
AAATGGACCACTGCTCCGTGCGGCTACAGTAAGGGCACGCGGCCGCCCACTATCGTCCC

SerLeuLeuSerProArgProIleSerTyrLeuLysGlySerSerGlyGlyProLeuLeu  
2101 GCAGCCTGCTGTGCCCCGGCCATTTCTACTTGAAAGGCTCCTCGGGGGGTCCGCTGT  
CGTCGGACGACAGCGGGGGCCGGGTAAAGGATGAACTTTCCGAGGAGCCCCCAGGCGACA

CysProAlaGlyHisAlaValGlyIlePheArgAlaAlaValCysThrArgGlyValAla  
2161 TGTGCCCCGCGGGGCGCGCGTGGGCATATTTAGGGCCGCGGTGTGCACCCGTGGAGTGG  
ACACGGGGCGCCCCGTGCGGCACCCGTATAAATCCGCGGCCACACGTGGGCACCTCACC

LysAlaValAspPheIleProValGluAsnLeuGluThrThrMetArgSerProValPhe  
2221 CTAAGCGGGTGGACTTTATCCCTGTGGAGAACCTAGAGACAACCATAGGTCCCCGGTGT  
GATTCGCCACCTGAAATAGGGACACCTCTTGATCTCTGTGGTACTCCAGGGGCCACA

ThrAspAsnSerSerProProValValProGlnSerPheGlnValAlaHisLeuHisAla  
2281 TCACGGATAACTCCTCTCCACCAAGTAGTGCCCCAGAGCTTCCAGGTGGCTCACCTCCATG  
AGTGCTATTGAGGAGAGGTGGTCATCACGGGGTCTCGAAGGTCCACCGAGTGGAGGTAC

ProThrGlySerGlyLysSerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLys  
2341 CTCCACAGGCAGCGGCAAAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATA  
GAGGGTGTCCGTGCGCTTTTCTGTGTTCCAGGGCCGACGTATACGTGAGTCCCGATAT

ValLeuValLeuAsnProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLys  
2401 AGGTGCTAGTACTCAACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGTACATGTCCA  
TCCACGATCATGAGTTGGGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGT

AlaHisGlyIleAspProAsnIleArgThrGlyValArgThrIleThrThrGlySerPro  
2461 AGGCTCATGGGATCGATCCTAACATCAGGACCGGGGTGAGAACAAATTACCACTGGCAGCC  
TCCGAGTACCCTAGCTAGGATTGTAGTCTGCCCCACTCTGTTAATGGTGACCGTCGG

IleThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyr  
2521 CCATCACGTACTCCACCTACGGCAAGTTCTTGCCGACGGCGGGTGTCTGGGGGGGCGCTT  
GGTAGTGATGAGGTGGATGCCGTTCAAGGAACGGCTGCCGCCACGAGCCCCCGCGAA

AspIleIleIleCysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGly  
2581 ATGACATAATAATTTGTGACGAGTGCCACTCCACGGATGCCACATCCATTTGGGCATCG  
TACTGTATTATTAACACTGCTCACGGTGAGGTGCTACGGTGAGGTAGAATACCCGTAGC

ThrValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThr  
2641 GCACTGTCTTGACCAAGCAGAGACTGCGGGGCGAGACTGGTTGTGCTCGCCACCGCCA  
CGTGACAGGAAGTGGTTCGTCTCTGACGCCCCGCTCTGACCAACACGAGCGGTGGCGGT

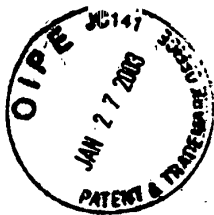
ProProGlySerValThrValProHisProAsnIleGluGluValAlaLeuSerThrThr  
2701 CCCCTCCGGGCTCCGTCACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCA  
GGGGAGGCCCGAGGCACTGACACGGGGTAGGGTTGTAGCTCCTCAACGAGACAGGTGGT

GlyGluIleProPheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHis  
2761 CCGGAGAGATCCCTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGAGAC  
GGCCTCTTAGGGAAAAATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCTCTG

LeuIlePheCysHisSerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeu  
2821 ATCTCATCTTCTGTCTTCAAGAAAGAGTGGCAGCAACTCGCCGCAAGCTGGTCCGAT  
TAGAGTAGAAGACAGTAAGTTTCTTCTTACGCTGCTTGAAGCGCGTTTCGACCAAGCGTA

GlyIleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGly  
2881 TGGGCATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGTCCGTATCCCGACCAAGCG  
ACCCGTAGTTACGGCACCGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGC

AspValValValAlaAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSer  
2941 GCGATGTTGTGCTCGTGGCAACCGATGCCCTCATGACCGGTATACCGGCGACTTCGACT  
CGCTACAACAGCAGCACCCTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGA



# FIG. 47D

ValIleAspCysAsnThrCysValThrGlnThrValAspPheSerLeuAspProThrPhe  
3001 CGGTGATAGACTGCAATACGTGTGTACCCAGACAGTCGATTTACGCTTGACCTACCT  
GCCACTATCTGACGTTATGCACACAGTGGGTCTGTGAGCTAAAGTCGGAACGGGATGGA

ThrIleGluThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArg  
3061 TCACCATTTGAGACAATCACGCTCCCCAGGATGCTGTCTCCGCACTCAACGTCGGGGCA  
AGTGGTAACCTCTGTTAGTGCAGGGGGTCTACGACAGAGGGCGTGAGTTGCAGCCCCGT

ThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGly  
3121 GGACTGGCAGGGGGAAGCCAGGCATCTACAGATTTGTGGCAGCGGGGAGCGCCCTCCG  
CCTGACCGTCCCCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGAGGC

MetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeu  
3181 GCATGTTGACTCGTCCGTCTCTGTGAGTGTATGACGCAGGCTGTGCTTGGTATGAGC  
CGTACAAGCTGAGCAGGCAGGAGACACTACGATACTGCGTCCGACACGAACCATCTCG

ThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProVal  
3241 TCACGCCCGCCGAGACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCG  
AGTGGGGCGGCTCTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGC

CysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAla  
3301 TGTGCCAGGACCATCTTGAAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATG  
ACACGGTCTCTGGTAGAACTTAAACCCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTAC

HisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGln  
3361 CCCACTTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCTTACCTGGTAGCGTACC  
GGGTGAAAGATAGGGTCTGTTTCTGTCTACCCCTCTTGAAGGAATGGACCATCGCATGG

AlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCys  
3421 AAGCCACCGTGTGCGCTAGGGCTCAAGCCCTCCCCATCGTGGGACCATGTGGAAGT  
TTCGGTGGCACACGCGATCCCGAGTTCGGGGAGGGGTAGCACCTGGTCTACACCTTCA

LeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAla  
3481 GTTTGATTGCGCTCAAGCCCACCCTCCATGGGCCAACCCCTGCTATACAGACTGGGCG  
CAAACATAAGCGGAGTTGCGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGC

ValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSer  
3541 CTGTTGAGAATGAAATCACCTGACGACCCAGTCACCAATATCATGACATGCATGT  
GACAAGTCTTACTTTAGTGGGACTGCGTGGGTGAGTGGTTTATGTAGTACTGTACGTACA

AlaAspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeu  
3601 CGGCCGACCTGGAGGTGCTCAGCAGCACCTGGGTGCTCGTTGGCGGCGTCTGGCTGCTT  
GCCGGCTGGACCTCCAGCAGTGTCTGTGGAACCCAGAGCAACGCCGAGGACCGACGAA

AlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeuSerGly  
3661 TGCCGCGTATTGCTGTCAACAGGCTGCGTGGTCATAGTGGGCAAGGTCGTCTTGTCCG  
ACCGGCGCATAACGGACAGTTGTCCGACGCACCACTATCACCCGTCCAGCAGAACAGGC

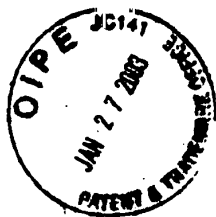
LysProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGlu  
3721 GGAAGCCGGCAATCATACCTGACAGGGAAGTCTCTACCGAGAGTTGATGAGATGGAAG  
CCTTCGGCCGTTAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTC

CysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGln  
3781 AGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGC  
TCACGAGAGTCGTGAATGGCATGTAGCTCGTTCCTACTACGAGCGGCTCGTCAAGTTCCG

LysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaVal  
3841 AGAAGGCCCTCGGCCTCTGACAGCCGCTCCGTCAGGCAGAGGTTATCGCCCTGCTG  
TCTTCCGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCAATAGCGGGGACGAC

GlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSer  
3901 TCCAGACCAACTGGCAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACCTTCATCA  
AGGTCTGGTTGACCGTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGT

GlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeu  
3961 GTGGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCAT  
CACCTATGTTATGAACGCCCGAACAGTTGCGACGGACCATTTGGGGCGGTAACGAAGTA



# FIG. 47E

MetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsn  
4021 TGATGGCTTTTACAGCTGCTGTACCAAGCCCACTAACCCTAGCCAAACCTCCTCTTCA  
ACTACCGAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGT

IleLeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheVal  
4081 ACATATTGGGGGGGTGGGTGGCTGCCAGCTCGCCGCCCCGGTGCCGCTACTGCCTTTG  
TGTATAACCCCCACCCACCGAGGGTCGAGCGGCGGGGGCCACGGCGATGACGGAAAC

GlyAlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAsp  
4141 TGGGCGCTGGCTTAGCTGGCGCCGCCATCGGCAAGTGTGGACTGGGGAAGGTCTCATAG  
ACCCGCGACCGAATCGACCGCGCGGTAGCCGTACAACCTGACCCCTTCCAGGAGTATC

IleLeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSer  
4201 ACATCCTTGCAGGGTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGA  
TGTAGGAACGTCCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACT

GlyGluValProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGly  
4261 GCGGTGAGGTCCCTCCACGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCG  
CGCCACTCCAGGGGAGGTGCTCCTGGACCAAGTATAGTGACGGGCGGTAGGAGAGCGGGC

AlaLeuValValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGlu  
4321 GAGCCCTCGTAGTCGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCG  
CTCGGGAGCATCAGCCGCACCAAGACACGTCGTTATGACGCGCCGTGCAACCGGGGCCGC

GlyAlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSer  
4381 AGGGGGCAGTGCAAGTGGATGAACCGGCTGATAGCCTTCGCTCCGGGGGGAACCATGTTT  
TCCCCGTCACGTCACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAA

ProThrHisTyrValProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSer  
4441 CCCCCACGCACTACGTGCCGAGAGCGATGCAAGCTGCCCGCGTCACTGCCATACTCAGCA  
GGGGGTGCGTGATGCACGGCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGT

LeuThrValThrGlnLeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThr  
4501 GCCTCACTGTAACCCAGCTCCTGAGGCGACTGCACCAAGTGGATAAGCTCGGAGTGTACCA  
CGGAGTGACATTGGGTGAGGACTCCGCTGACGTGGTCACCTATTGAGCCTCACATGGT

ProCysSerGlySerTrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAsp  
4561 CTCCATGCTCCGGTTCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCG  
GAGGTACGAGGCCAAGGACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACCTCGC

PheLysThrTrpLeuLysAlaLysLeuMetProGlnLeuProGlyIleProPheValSer  
4621 ACTTTAAGACCTGGCTAAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCCTTTGTGT  
TGAAATTCTGGACCGATTTTCGATTGAGTACGGTGTGACGGACCCTAGGGGAAACACA

CysGlnArgGlyTyrLysGlyValTrpArgValAspGlyIleMethHisThrArgCysHis  
4681 CCTGCCAGCGCGGGTATAAGGGGGTCTGGCGAGTGGACGGCATGACACTCGTGCC  
GGACGGTCGCGCCCATATTCCCCAGACCCTCACCTGCCGTAGTACGTGTGAGCGACGG

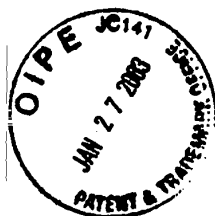
CysGlyAlaGluIleThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArg  
4741 ACTGTGGAGCTGAGATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCCTA  
TGACACCTCGACTCTAGTGACCTGTACAGTTTTTGCCTGCTACTCTAGCAGCCAGGAT

ThrCysArgAsnMetTrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCys  
4801 GGACCTGCAGGAACATGTGGAGTGGGACCTTCCCCATTAAATGCCTACACCACGGGCCCT  
CCTGGACGTCTTGTACACCTCACCTGGAAAGGGTAATTACGGATGTGGTGCCCGGGGA

ThrProLeuProAlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyr  
4861 GTACCCCCCTTCTGCGCCGAACCTACACGTTGCGCTATGGAGGGTGTCTGCAGAGGAAT  
CATGGGGGGAAGGACGCGGCTTGATGTGCAAGCGGATACCTCCCACAGACGTCTCCTTA

ValGluIleArgGlnValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeu  
4921 ATGTGGAGATAAGGCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATC  
TACACCTCTATTCCGTCCACCCCTGAAGGTGATGCACTGCCATACTGATGACTGTAG

LysCysProCysGlnValProSerProGluPhePheThrGluLeuAspGlyValArgLeu  
4981 TCAAATGCCCGTGCGAGGTCCCATCGCCGAATTTTTACAGAAATGGACGGGGTGCGCC  
AGTTTACGGGCACGGTCCAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGG



# FIG. 47F

HisArgPheAlaProProCysLysProLeuLeuArgGluGluValSerPheArgValGly  
5041 TACATAGGTTTGC GCCCCTGCAAGCCCTTGCTGCGGAGGAGGTATCATTAGAGTAG  
ATGTATCCAAACGCGGGGGACGTTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATC

LeuHisGluTyrProValGlySerGlnLeuProCysGluProGluProAspValAlaVal  
5101 GACTCCACGAATACCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCG  
CTGAGGTGCTTATGGGCCATCCAGCGTTAATGGAACGCTCGGGCTTGGCTGCACCGGC

LeuThrSerMetLeuThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeu  
5161 TGTTGACGTCCATGCTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGCGAAGGT  
ACAACTGCAGGTACGAGTGACTAGGGAGGGTATATTGTCGTCTCCGCGGCCGCTTCCA

AlaArgGlySerProProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSer  
5221 TGGCGAGGGGATCACCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCAT  
ACCGCTCCCTAGTGGGGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTA

LeuLysAlaThrCysThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsn  
5281 CTCTCAAGGCAACTTGCACCGCTAACCATGACTCCCTGATGCTGAGCTCATAGAGGCCA  
GAGAGTTCGGTTGAACGTGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGT

LeuLeuTrpArgGlnGluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysVal  
5341 ACCTCCTATGGAGGCAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAAACAAAG  
TGAAGATACCTCCGTCTCTACCCGCCGTTGTAGTGGTCCCACTCAGTCTTTTGTTC

ValIleLeuAspSerPheAspProLeuValAlaGluGluAspGluArgGluIleSerVal  
5401 TGGTGATTCTGGACTCCTTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCG  
ACCACTAAGACCTGAGGAAGCTAGGCGAACACCGCCTCCTCCTGCTGCCCTCTAGAGGC

ProAlaGluIleLeuArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArg  
5461 TACCCGAGAAATCCTGCGGAAGTCTCGGAGATTGCGCCAGGCCCTGCCGTTTGGGCGC  
ATGGGCGTCTTTAGGACGCCCTCAGAGCCTTAAGCGGGTCCGGGACGGGCAAAACCGCG

ProAspTyrAsnProProLeuValGluThrTrpLysLysProAspTyrGluProProVal  
5521 GGCGGACTATAACCCCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACACCTG  
CCGGCTGATATTGGGGGGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGAC

ValHisGlyCysProLeuProProProLysSerProProValProProArgLysLys  
5581 TGGTCCATGGCTGTCCGCTTCCACCTCAAAGTCCCTCCTGTGCCTCCGCTCGGAAGA  
ACCAGGTACCGACAGGCGAAGGTGGAGGTTTCAGGGGAGGACACGGAGCGGAGCCTCT

ArgThrValValLeuThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArg  
5641 AGCGGACGGTGGTCTCACTGAATCAACCTATCTACTGCCTTGGCCGAGCTCGCCACCA  
TCGCCGCCACACGAGTGACTTAGTTGGGATAGATACGGAACCGGCTCGAGCGGTGGT

SerPheGlySerSerSerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGlu  
5701 GAAGCTTTGGCAGCTCCTCAACTTCGGCATTACGGGCGACAATACGACAACATCCTCTG  
CTTCGAAACCGTCGAGGAGTTGAAGGCCGTAATGCCGCTGTTATGCTGTTGTAGGAGAC

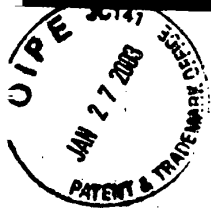
ProAlaProSerGlyCysProProAspSerAspAlaGluSerTyrSerSerMetProPro  
5761 AGCCGCCCTTCTGGCTGCCCCCGGACTCCGACGCTGAGTCTATTCTCCATGCCCC  
TCGGGCGGGGAAGACCGACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGG

LeuGluGlyGluProGlyAspProAspLeuSerAspGlySerTrpSerThrValSerSer  
5821 CCCTGGAGGGGGAGCCTGGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTA  
GGGACCTCCCCCTCGAACCCCTAGGCTAGAATCGCTGCCAGTACCAAGTTGCCAGTCAT

GluAlaAsnAlaGluAspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeu  
5881 GTGAGGCCAACGCGGAGGATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCAC  
CACTCCGGTTGCGCTCTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTG

ValThrProCysAlaAlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeu  
5941 TCGTCACCCCGTGCGCCGCGGAAGAACAGAACTGCCCATCAATGCACTAAGCAACTCGT  
AGCAGTGGGGCACGCGGCGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCTGTGAGCA

LeuArgHisHisAsnLeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLys  
6001 TGCTACGTACCCACAATTTGGTGTATTCCACCACCTCACGAGTGCTTGCCAAAGGCAGA  
ACGATGCAGTGGTGTTAAACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGCTCT



# FIG. 47G

LysValThrPheAspArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGlu  
6061 AGAAAGTCACATTTGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGG  
TCTTTCAGTGTAACCTGTCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCC

ValLysAlaAlaAlaSerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSer  
6121 AGGTTAAAGCAGCGGCGTCAAAAGTGAAGGCTAAGTTGCTATCCGTAGAGGAAGCTTGCA  
TCCAATTCGTCGCCGAGTTTTCACTCCGATTGAACGATAGGCATCTCTTCGAACGT

LeuThrProProHisSerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCys  
6181 GCCTGACGCCCCACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTT  
CGGACTGCGGGGGTGTGAGTCGGTTTAGGTTCAAACCAATACCCGTTTTCTGACGGCAA

HisAlaArgLysAlaValThrHisIleAsnSerValTrpLysAspLeuGluAspAsn  
6241 GCCATGCCAGAAAGGCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACA  
CGGTACGGTCTTTCGGCATTGGGTGTAGTTGAGGCACACCTTCTGGAAGACCTTCTGT

ValThrProIleAspThrThrIleMetAlaLysAsnGluValPheCysValGlnProGlu  
6301 ATGTAACACCAATAGACACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTGAGCCTG  
TACATTGTGGTTATCTGTGATGGTAGTACCGATTCTTGCTCCAAAGACGCAAGTCGGAC

LysGlyGlyArgLysProAlaArgLeuIleValPheProAspLeuGlyValArgValCys  
6361 AGAAGGGGGGTCGTAAGCCAGCTCGTCTCATCGTGTCCCCGATCTGGGCGTGGCGGTGT  
TCTTCCCCCAGCATTGGTTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGACA

GluLysMetAlaLeuTyrAspValValThrLysLeuProLeuAlaValMetGlySerSer  
6421 GCGAAAAGATGGCTTTGTACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCT  
CGCTTTTCTACCGAAACATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCCTTCA

TyrGlyPheGlnTyrSerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSer  
6481 CCTACGGATTCCAATACTCACCAGGACAGCGGGTTGAATTCCTCGTGAAGCGTGGAAAT  
GGATGCCAAGGTTATGAGTGGTCTGTCGCCAACTTAAGGAGCAGGTTCCGACCTTCA

LysLysThrProMetGlyPheSerTyrAspThrArgCysPheAspSerThrValThrGlu  
6541 CCAAGAAAACCCCAATGGGGTTCTCGTATGATACCCGCTGCTTGGACTCCACAGTCACTG  
GGTCTTTTGGGGTTACCCCAAGAGCATACTATGGGCGACGAACTGAGGTGTCAAGTGC

SerAspIleArgThrGluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArg  
6601 AGAGCGACATCCGTACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCAAGCCC  
TCTCGCTGTAGGCATGCCTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCCGG

ValAlaIleLysSerLeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArg  
6661 GCGTGGCCATCAAGTCCCTCACCAGAGGGCTTTATGTTGGGGGCCCTTTACCAATTCAA  
CGCACCGGTAGTTCAGGGAGTGGCTCTCCGAAATAACCCCGGGAGAAATGGTTAAGTT

GlyGluAsnCysGlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGly  
6721 GGGGGGAGAACTGCGGCTATCGCAGGTGCCGCGCGAGCGGCTACTGACAAGTACGCTGTG  
CCCCCTCTTGACGCCGATAGCGTCCACGGCGGCTCGCCGATGACTGTTGATCGACAC

AsnThrLeuThrCysTyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAsp  
6781 GTAACACCCTCACTTGCTACATCAAGGCCCGGGCAGCCTGTGAGCCGCGAGGGCTCCAGG  
CATTGTGGGAGTGAACGATGTAGTTCGGGGCCGTCGGACAGCTCGGCGTCCCGAGGTCC

CysThrMetLeuValCysGlyAspAspLeuValValIleCysGluSerAlaGlyValGln  
6841 ACTGCACCATGCTCGTGTGTGGCGACGACTTAGTCTGTTATCTGTGAAAGCGCGGGGGTCC  
TGACGTGGTACGAGCACACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCAGG

GluAspAlaAlaSerLeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProPro  
6901 AGGAGGACGCGGCGAGCCTGAGAGCCTTACGGAGGCTATGACCAAGTACTCCGCCCCC  
TCTCTGCGCCGCTCGGACTCTCGGAAGTGCTCCGATACTGGTCCATGAGCGGGGGG

GlyAspProProGlnProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnVal  
6961 CTGGGGACCCCCACAACAGAAATACGACTTGGAGCTCATAACATCATGCTCCTCCAAGC  
GACCCCTGGGGGGTGTGGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGC

SerValAlaHisAspGlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThr  
7021 TGTAGTCGCCCACGACGGCGCTGGAAAGAGGGTCTACTACCTACCCGTTGACCTACAA  
ACAGTCAGCGGGTGTGTCGCGACCTTCTCCAGATGATGGAGTGGGCACTGGGATGTT

FIG. 47H

7081 ProLeuAlaArgAlaAlaIrpGluThrAlaArgHisThrProValAsnSerTrpLeuGly  
CCCCCTCGCGAGAGCTGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAG  
GGGGGGAGCGCTCTCGACGCACTCTGTCGTTCTGTGTGAGGTCAAGGACCGATC

7141 AsnIleIleMetPheAlaProThrLeuIrpAlaArgMetIleLeuMetThrHisPhe  
GCAACATATCATGTTGCCCCACACTGTGGCCGAGGATGATACTGATGACCAATTTCT  
CGTTGATTAGTACAACAGGGGGGTGTGACACCCGCTCTACTATGACTACTGGGTAAGA

7201 SerValLeuIleAlaArgAspGlnLeuGlnAlaLeuAspCysGluIleTyGlyAla  
TTAGCGTCCCTTATAGCCAGGGGACCAAGCTTGAAACAAGGCCCTCGATTGCGAGATCTACGGGG  
AATCGCAGGAATATCGGTCCCTGGTCGAACCTTGTCCGGGAGCTAACGCTCTAGATGCCCC

7261 CysTyrSerIleGluProLeuAspLeuProIleIleGlnArgLeu  
CCTGCTACTCCATAGAACCACTTGATCTACCTCCAATCATTCAAGACTC  
GGACGATGAGGTATCTTGGTGAACTAGATGGAAGTTAGTAAGTTTCTGAG





FIG. 48

ProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSerTyrGly  
 1CTCCAGACCCCGTGGTGGTGGACGACGACGAGTGGGGCGGCTACCTACAGCTGG  
 GAGGTCGGGGGCACCAACCCTGCTGGCTGTCCAGCCCGCGGATGATGTGACCC  
 GluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsnTyrPhe  
 61GTGAAATGATACGAGCGTCTTCCTTAACAATACAGGCCACCGCTGGCAATTGT  
 CACTTTACTATGCCCTGCAGACGAGAAATTGTATGTCGCGTGCGCAACCTTAACA  
 GlyCysThrTyrMetAsnSerThrGlyPheThrLysValCysGlyAlaProProCysVal  
 121TCGGTTGACCTGGATGACTCACTGATTCACCAAGTGTGCGAGCGCTCTGTG  
 AGCCAACATGGAACCTACTGAGTTGACCTAAGTGGTTTCACACGCCCTCGCGAGAACAC  
 IleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLysHisPro  
 181TCATCGGAGGGCGGGCAACAACACCTGCACCTGCCCACTGATGCTTCCGCAAGCATC  
 AGTAGCCTCCCGCCCGTGTGTGTGGACGTGACGGGGTGACTAACGAAGCGTTCGTAG  
 AspAlaThrTyrSerArgCysGlySerGlyProTyrPleuThrProArgCysLeuValAsp  
 241CGGAGCCACATACTCTCGGTGCGGCTCCGCTCCCTGGCTCACACCCAGGTGCCCTGTCG  
 GCTCGCGTGTATGAGAGCCACGCCGAGGCCAGGACCGAGTGTGGTCCACGGACCAAC  
 TyrProTyrArgLeuTyrPheHisTyrProCysThrIleAsnTyrThrIlePheLysIleArg  
 301ACTACCCGTATAGGCTTTGGCATTTATCCTTGTACCATCAACTACACCATATTTAAATCA  
 TGATGGCATATCCGAACCGTAATAGGAACATGTAGTTGATGTGTTAATAATTTAGT  
 MetTyrValGlyGlyValGlyHisArgLeuGlyAlaAlaCysAsnTyrPheArgGlyGly  
 361GGATGTACGTGGAGGGGTGAGCACAGGCTGGAAGCTGCCCACTGACGCGGGCGG  
 CTAACATGCACCCCTCCCAAGCTCGTGTCCGACCTTCGACGGACGTTGACCTGCCCGCGC  
 -----Overlap with 12f-----  
 ArgCysAspLeuGlyAspArgAspArgSerGlyLeuSerProLeuLeuLeuThrThrThr  
 421AACGTTGCGATCTGGAAGACAGGACAGGTCCGAGCTCAGCCCGTTACTGCTGACCACTA  
 TTGCAACGCTAGACCTTCTGTCTCCCTGTCCAGGCTCGAGTCGGGCAATGACGACTGGTAT  
 GlnTyrGlnValLeuProCysSerPheThrThrLeuProAlaLeuSerThrGlyLeu  
 481CACAGTGGCAGGTCCTCCCGTGTCTTCACAAACCTGCCAGCCTGTGTCCACCGGCTCA  
 GTGTCAACCGTCCAGGAGGGCACAAAGAGTGTGGACGGTCCGAACAGGTGCGCGGAGT



FIG. 49

LeuphetYrHISHisLysPheAsnSerSergLysProGluArgLeuAlaSerCysArg  
1 GCTTTCTATCACCACAGTTCACCTCTCAGGCTGCTCCTGAGAGCTAGCCAGCTGCCG  
CGAAAGATAGTGGTGTTCAGTTGAGAGTCCGACAGGACTCTCCGATCGGTCCGACGGC  
ProLeuThrAspPheAspGlnGlyTyrGlyProIleSerTyrAlaAsnGlySergLysPro  
61 ACCCTTACCGATTGTGACCAAGGCTGGGCCCTATCAGTTATGCCAACGGAAGCGGCC  
TGGGAATGGCTAAACTGGTCCCGACCCCGGATAGTCAATACGGTTGCCCTCGCCGGG  
AspGlnAlaGProTyrCysTrpHisTyrProProLysProCysGlyIleValProAlaLys  
121 CGACCAAGCGCCCTACTGCTGGCACTACCCCAAAACCTTGGGTATTGTCGCCGAA  
GCTGGTCGGGGGATGACGACCGTGA TGGGGGTTTGGAAACGCCATTAACACAGGGCGCTT  
---Overlap with 131---  
SerValCysGlyProValTyrCysPheThrProSerProValValVal  
181 GAGTGTGTGGTCCGGTATATTGCTTCACTCCAGCCCGTGGTGGG  
CTCACACACACAGGCCATATAACGAAGTGAGGTCGGGGCACCAACCACCC



FIG. 50

LeuValMetAlaGlnLeuLeuArgIleProGlnAlaIleLeuAspMetIleAlaGlyAla  
 1 TTGGTATGGCTCAGCTGCTCCGGATCCACAGCCATCTTGACATGATCGCTGGTCT  
 AACCATTACCGAGTCGACGAGGCCCTAGGGTGTTCGGTAGAACCTGTACTAGCGACACGA  
 HisTrpGlyValLeuAlaGlyIleAlaTyrrPheSerMetValGlyAsnTrpAlaLysVal  
 61 CACTGGGAGTCTCGCGGGCATAGCGTATTTCTCCATGGTGGGACTGGCGAAGTTC  
 GTGACCCCTCAGGACCGCCCGTATCGCATAAAGAGGTACCACCCCTTGACCCGCTTCCAG  
 LeuValValLeuLeuLeuPheAlaGlyValAlaSpAlaGluThrHisValThrGlyGlySer  
 121 CTGGTAGTGTGCTGCTATTGCGCGCGTCGACCGGAAACCCACGTCACCGGGGAAGT  
 GACCATCACGACGACGATAAACGGCCGACGCTGCGCCTTTGGGTGCAGTGGCCCCCTTCA  
 AlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLysGlnAsnVal  
 181 GCCGGCCACACTGTGTCTGATTTGTTAGCCTCCTCGCACAGCGGCCAAGCAGAACGTC  
 CGGCCGGTGTGACACAGACCTAAACAATCGGAGAGCGGTGTCGCCGCTTCTTGACG  
 GlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsnCysAsnAsp  
 241 CAGCTGATCAACACACCAACGGCAGTTGGCACCTCAATAGCACGGCCCTGAATGCAATGAT  
 GTCGACTAGTTGTGGTTCGCCGTCAACCGTGGAGTTATCGTGCCGGGACTTGACGTTACTA  
 SerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrrHisHisLysPheAsnSerSerGly  
 301 AGCCTCAACACCGCGCTGTGGCAGGCTTTCTATCAACCAAGTTCAACTCTTCAGGC  
 TCGGAGTTGTGGCCGACCAACCGTCCCGAAAGATAGTGGTGTCAAGTTGAGAAAGTCCG  
 -----Overlap with 26j-----  
 -----Overlap with K9-1-----  
 CysProGluArgLeuAlaSerCysArgPro  
 361 TGTCTGAGAGGCTAGCCAGCTGCCGACCCC  
 ACAGGACTCTCCGATCGGTGACGCGCTGGGG  
 -----

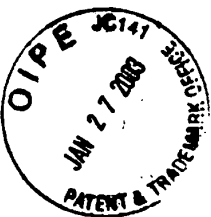




FIG. 51

GlnGlyCysAsnCysSerIleTyrProGlyHisIleThrGlyHisArgMetAlaTrpAsp  
1CGCAAGGTGCAATTGCTCTATCTATCCCGCCATATAACGGGTACCGCATGGCATGGG  
GCGTCCCAACGTTAACGAGATAGATAGGCGCGGTATATTGCCAGTGGCGTACCGTACCC

MetMetMetAsnTrpSerProThrAlaLeuValMetAlaGlnLeuLeuArgIlePro  
61ATATGATGATGAACCTGGTCCCTACGACGGCGTTGGTAATGGCTCAGCTGCTCCGGATCC  
TATACTACTTGTACCAAGGGATGCTGCCGCAACCATTACCGAGTCGACGAGCCCTAGG

GlnAlaIleLeuAspMetIleAlaGlyAlaHisTrpGlyValLeuAlaGlyIleAlaTyr  
121CACAAAGCCATCTTGGACATGATCGCTGGTGCTCACTGGGAGTCCCTGGGGCATAGCGT  
GTGTTCCGGTAGAACCTGTACTAGCGACCAAGTAGTACCCCTCAGGACCGCCCGTATCGCA

-----Overlap with CA59a-----  
PheSerMetValGlyAsnTrpAlaLysValLeuValValLeuLeuPheAlaGlyVal  
181ATTTCCTCCATGGTGGGAACTGGGCGAAGTCCCTGGTAGTGTGCTGCTATTGCCGGCG  
TAAAGAGGTACCAACCCCTTGACCCGCTTCCAGGACCATCACGACGATAAACGGCCGC

-----  
AspAlaGluThrHisValThrGly  
241TCGACGCGGAAACCCACGTCACCGGGG  
AGCTGCGCCCTTTGGGTGCAGTGGCCCC

FIG. 52

CysTrpValAlaMetThrProThrValAlaThrArgAspGlyLysLeuProAlaThrGln  
1 GTGTGGTGGCGATGACCCCTACGGTGCCACCAAGGATGCCAACTCCCGCAGCCA  
CACACCCACCCTACTGGGATGCCACCGGTGTCCTACCGTTTGAGGGCGCTGCGT

LeuArgArgHisIleAspLeuValGlySerAlaThrLeuCysSerAlaLeuTyrVal  
61 GCTTCGACGTCACATCGATCTGCTTGCGGAGCGCCACCTCTGTTGCGCCCTACGT  
CGAAGCTGCAGTGTAGCTAGACGAACAGCCCTCGCGGTGGAGACAAGCCGGAGATGCA

GlyAspLeuCysGlySerValPheLeuValGlyGlnLeuPheThrPheSerProArgArg  
121 GGGGACCTATGCGGGTCTGCTTCTTGTCGGCCAACGTTCACCTTCTCTCCAGCG  
CCCCCTGGATACGCCCAAGACAGAAAGAACAGCCGGTTGACCAAGTGGAAGAGAGGCTCCG

HisTrpThrThrGlnGlyCysAsnCysSerIleTyrProGlyHisIleThrGlyHisArg  
181 CCACTGGACGACGCAAGGTGCAATTGCTCTATCTATCCCGGCATATAACGGGTACCG  
GGTGACCTGCTGCGTTCCAAACGTTAACGAGATAGTAGGGCCGCTATATTGCCACGTGCC

-----Overlap with CA84a-----  
MetAlaTrpAspMetMetMetAsnTrpSerProThrThrAlaLeuValValAlaGlnLeu  
241 CATGGCATGGGATATGATGATGAACCTGTCCTACGACGCGGTGGTAGTGCTCAGCT  
GTACCGTACCTATACTACTTGAACCAAGGGATGCTGCCGCAACCATCACCAGAGTCGA

-----  
LeuArgIleProGlnAla  
301 GCTCCGATCCACAGCC  
CGAGGCCCTAGGGTGTTCGG

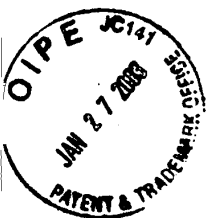


FIG. 53

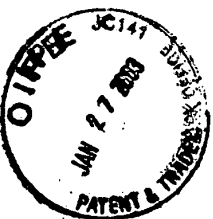
SerThrGlyLeuTyrHisValThrAsnAspCysProAsnSerSerIleValTyrGluAla  
1CTCCACGGGGCTTTACCAACGTCACCAATGATGCCCTAAGTATGTTGTAACGAGGC  
GAGGTGCCCCGAAATGGTGCAAGTGGTTACTAACGGGATTGAGCTCATACACATGCTCCG

AlaAspAlaIleLeuHisThrProGlyCysValProCysValArgGluGlyAsnAlaSer  
61GGCCGATGCCATCCTGCACACTCCGGGGTGCGTCCCTTGCGTTGAGGGCAACGCTC  
CCGGCTACGGTAGGACGTGTGAGGCCCCACGCAAGGAACCAAGCACTCCCGTTGCCGAG

ArgCysTrpValAlaMetThrProThrValAlaThrArgAspGlyLysLeuProAlaThr  
121GAGGTGTGGGGTGCGATGACCCCTACGGTGCCACCAAGGATGGCAAACTCCCCGGAC  
CTCCACAACCCACCGCTACTGGGGATGCCACCGGTGCTCCCTACCCTTGAGGGGGCTG

-----Overlap with CA156-----  
GlnLeuArgArgHisIleAspLeuLeuValGlySerAlaThrLeuCysSerAlaLeuTyr  
181GCAGCTTCGACGTCACATCGATCTGCTTGTGGGAGCGCTACCCCTCTGTTGGCCCTTA  
CGTCGAAGCTGCAGTGTAGCTAGACGAACAGCCCTCGGATGGGAGACCAAGCCGGGAGAT

-----  
ValGlyAspLeuCysGlySerValPheLeu  
241CGTGGGGGACTGTGCGGGTCTGTCTTCTTG  
GCACCCCTGAACACGCCCAAGACAGAAGAAC



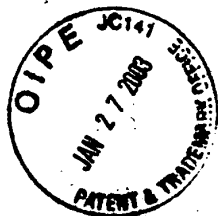


FIG. 54A

ArgSerArgAsnLeuGlyLysValIleAspThrLeuThrCysGlyPheAlaAspLeuMet  
1 AGGTCGCGCAATTTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCATG  
TCCAGCGCGTTAAACCCATTCCAGTAGCTATGGGAATGCACGCCGAAGCGGCTGGAGTAC

GlyTyrIleProLeuValGlyAlaProLeuGlyGlyAlaAlaArgAlaLeuAlaHisGly  
61 GGGTACATACCGCTCGTCGGCGCCCTCTTGGAGGCGCTGCCAGGGCCCTGGCGCATGGC  
CCCATGTATGGCGAGCAGCCGCGGGGAGAACCTCCGCGACGGTCCCGGGACCGCGTACCG

ValArgValLeuGluAspGlyValAsnTyrAlaThrGlyAsnLeuProGlyCysSerPhe  
121 GTCCGGGTTCTGGAAGACGGCGTGAACATGCAACAGGGAACCTTCCTGGTTGCTCTTTC  
CAGGCCCAAGACCTTCTGCCGCACTTGATACGTTGTCCCTTGGAAGGACCAACGAGAAAG

SerIlePheLeuLeuAlaLeuLeuSerCysLeuThrValProAlaSerAlaTyrGlnVal  
181 TCTATCTTCTTCTGGCCCTGCTCTTGTCTTGACTGTGCCCGCTTCGGCCTACCAAGTG  
AGATAGAAGGAAGACCGGGACGAGAGAACGAACTGACACGGGCGAAGCCGGATGGTTCAC

ArgAsnSerThrGlyLeuTyrHisValThrAsnAspCysProAsnSerSerIleValTyr  
241 CGCAACTCCACGGGGCTTTACCACGTACCAATGATTGCCCTAACTCGAGTATTGTGTAC  
GCGTTGAGGTGCCCCGAAATGGTGCAGTGTTACTAACGGGATTGAGCTCATAACACATG

GluAlaAlaAspAlaIleLeuHisThrProGlyCysValProCysValArgGluGlyAsn  
301 GAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGCCTCCCTTGCGTTGCTGAGGGCAAC  
CTCCGCCGCTACGGTAGGACGTGTGAGGCCCCACGCAAGGGAACGCAAGCACTCCCGTTG

AlaSerArgCysTrpValAlaMetThrProThrValAlaThrArgAspGlyLysLeuPro  
361 GCCTCGAGGTGTTGGGTGGCGATGACCCCTACGGTGGCCACCAGGGATGGCAAACCTCCCC  
CGGAGCTCCACAACCCACCGCTACTGGGGATGCCACCGGTGGTCCCTACCGTTTGAGGGG

AlaThrGlnLeuArgArgHisIleAspLeuLeuValGlySerAlaThrLeuCysSerAla  
421 GCGACGCAGCTTCGACGTACATCGATCTGCTTGTGCGGAGCGCCACCCTCTGTTGCGCC  
CGCTGCGTCGAAGCTGCAGTGTAGCTAGACGAACAGCCCTCGCGGTGGGAGACAAGCCGG

LeuTyrValGlyAspLeuCysGlySerValPheLeuValGlyGlnLeuPheThrPheSer  
481 CTCTACGTGGGGGACCTATGCGGGTCTGTCTTTCTTGTGCGCCAACTGTTACCTTCTCT  
GAGATGCACCCCTGGATACGCCAGACAGAAAGAACAGCCGGTTGACAAGTGGAAGAGA

ProArgArgHisTrpThrThrGlnGlyCysAsnCysSerIleTyrProGlyHisIleThr  
541 CCCAGGCGCCACTGGACGACGCAAGGTTGCAATTGCTCTATCTATCCCGGCCATATAACG  
GGGTCCGCGGTGACCTGCTCCGTTCCAACGTTAACGAGATAGATAGGGCCGGTATATTGC

GlyHisArgMetAlaTrpAspMetMetMetAsnTrpSerProThrThrAlaLeuValMet  
601 GGTCAACGATGGCATGGGATATGATGATGAAGTGGTCCCCTACGACGGCGTTGGTAATG  
CCAGTGGCGTACCGTACCCTATACTACTTGAACAGGGGATGCTGCCGCAACCATTAC

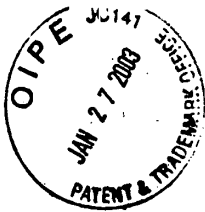


FIG. 54B

AlaGlnLeuLeuArgIleProGlnAlaIleLeuAspMetIleAlaGlyAlaHisTrpGly  
661 GCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGGCTCACTGGGGA  
CGAGTCGACGAGGCCAGGGTGTTCGGTAGAACCTGTACTAGCGACCACGAGTGACCCCT

ValLeuAlaGlyIleAlaTyrPheSerMetValGlyAsnTrpAlaLysValLeuValVal  
721 GTCCTGGCGGGCATAGCGTATTTCTCCATGGTGGGGAAGTGGGCGAAGGTCCTGGTAGTG  
CAGGACCGCCGTATCGCATAAAGAGGTACCACCCCTTGACCCGCTTCAGGACCATCAC

LeuLeuLeuPheAlaGlyValAspAlaGluThrHisValThrGlyGlySerAlaGlyHis  
781 CTGCTGCTATTTGCCGGCGTCGACGCGGAAACCCACGTCACCGGGGGAAGTGGCGGCAC  
GACGACGATAAACGGCCGACGCTGCGCCTTTGGGTGCAGTGGCCCCCTTCAGGCCGGTG

ThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLysGlnAsnValGlnLeuIle  
841 ACTGTGTCTGGATTTGTAGCCTCCTCGCACCAGGCGCCAAAGCAGAAGCTCCAGCTGATC  
TGACACAGACCTAAACAATCGGAGGAGCGTGGTCCGCGGTTCTGCTTCAGGTCGACTAG

AsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsnCysAsnAspSerLeuAsn  
901 AACACCAACGGCAGTTGGCACCTCAATAGCACGGCCCTGAAGTGAATGATAGCTCAAC  
TTGTGGTTGCCGTCACCGTGGAGTTATCGTGCCGGGACTTGACGTTACTATCGGAGTTG

ThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsnSerSerGlyCysProGlu  
961 ACCGGCTGGTTGGCAGGGCTTTCTATCACCACAAGTTCAACTCTTCAGGCTGTCTGAG  
TGGCCGACCAACCGTCCCGAAAAGATAGTGGTGTCAAGTTGAGAGTCCGACAGGACTC

ArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGlyTrpGlyProIleSerTyr  
1021 AGGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACCAGGGCTGGGGCCCTATCAGTTAT  
TCCGATCGGTCGACGGCTGGGGAATGGCTAAACTGGTCCCAGCCCCGGGATAGTCAATA

AlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHisTyrProProLysProCys  
1081 GCCAACGGAAGCGGCCCCGACCGAGCGCCCTACTGCTGGCACTACCCCCAAAACCTTGC  
CGGTTGCCTTCGCCGGGGCTGGTGCGGGGATGACGACCGTGATGGGGGGTTTGGAAAG

GlyIleValProAlaLysSerValCysGlyProValTyrCysPheThrProSerProVal  
1141 GGTATTGTGCCCGCAAGAGTGTGTGTGGTCCGGTATATTGCTTCACTCCAGCCCCGTG  
CCATAACACGGGCGCTTCTCACACACACAGGCCATATAACGAAGTGAGGGTCGGGGCAC

ValValGlyThrThrAspArgSerGlyAlaProThrTyrSerTrpGlyGluAsnAspThr  
1201 GTGGTGGGAACGACCGACAGGTCGGGCGCGCCACCTACAGCTGGGGTGAAAATGATACG  
CACCACCTTGCTGGCTGTCCAGCCGCGCGGGTGGATGTCGACCCCACTTTTACTATGC

AspValPheValLeuAsnAsnThrArgProProLeuGlyAsnTrpPheGlyCysThrTrp  
1261 GACGTCTTCGTCTTAACAATACAGGCCACCGCTGGGCAATTGGTTGCGTTGTACCTGG  
CTGCAGAAGCAGGAATTGTTATGGTCCGGTGGCGACCCGTTAACCAAGCCAACATGGACC

MetAsnSerThrGlyPheThrLysValCysGlyAlaProProCysValIleGlyGlyAla  
1321 ATGAAGTCAACTGGATTACCAAAGTGTGCGGAGCGCCTCTTGTGTATCGGAGGGGCG  
TACTTGAGTTGACCTAAGTGGTTTACACGCTCGCGGAGGAACACAGTAGCCTCCCCGC

GlyAsnAsnThrLeuHisCysProThrAspCysPheArgLysHisProAspAlaThrTyr  
1381 GGCAACAACACCCTGCACTGCCCACTGATTGCTTCCGCAAGCATCCGGACGCCATAC  
CCGTTGTTGTGGGACGTGACGGGGTACTAACGAAGGCGTTGCTAGGCCCTGCGGTGTATG

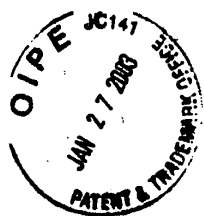
SerArgCysGlySerGlyProTrpIleThrProArgCysLeuValAspTyrProTyrArg  
1441 TCTCGGTGC66CTCCGGTCCCTGGATCACACCAAGGTGCCTGGTCACTACCCGTATAGG  
AGAGCCACGCCAGGCCAGGGACCTAGTGTGGGTCCACGGACCACTGATGGGCATATCC

LeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLysIleArgMetTyrValGly  
1501 CTTTGGCATTATCCTTGTACCATCACTACACCATATTTAAATCAGGATGTACGTGGGA  
GAAACCGTAATAGGAACATGGTAGTTGATGTGGTATAAATTTAGTCTACATGACCCCT

GlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArgGlyGluArgCysAspLeu  
1561 GGGGTGAAACACAGGCTGGAAGCTGCCTGCAACTGGACGCGGGGCGAACGTTGCGATCTG  
CCCCAGCTTGTGTCCGACCTTCACGGACGTTGACCTGCGCCCCGCTTGCAACGCTAGAC

GluAspArgAspArgSerGluLeuSerProLeuLeuLeuThrThrThrGlnTrpGlnVal  
1621 GAAGACAGGGACAGGTCGAGCTCAGCCGTTACTGTGACCACTACACAGTGGCAGGTC  
CTTCTGTCCCTGTCCAGGCTCGAGTCGGGCAATGACGACTGGTGATGTGTACCGTCCAG





# FIG. 54C

LeuProCysSerPheThrThrLeuProAlaLeuSerThrGlyLeuIleHisLeuHisGln  
1681 CTCCCGTGTTCCTTCAACCCCTACCAGCCTTGCCACCGGCCTCATCCACCTCCACCAG  
GAGGGCACAAGGAAGTGTGGGATGGTGGGAACAGGTGGCCGGAGTAGGTGGAGGTGGTC

AsnIleValAspValGlnTyrLeuTyrGlyValGlySerSerIleAlaSerTrpAlaIle  
1741 AACATTGTGGACGTGCAGTACTTGTACGGGGTGGGGTCAAGCATCGCGTCTGGGCCATT  
TTGTAACACCTGCACGTGATGAACATGCCCCACCCAGTTCGTAGCGCAGGACCCGGTAA

LysTrpGluTyrValValLeuLeuPheLeuLeuAlaAspAlaArgValCysSerCys  
1801 AAGTGGGAGTACGTGTTCTCCTGTTCTCTGCTTGACAGACGCGCGCTGCTCCTGCTG  
TTCACCCTCATGCAGCAAGAGGACAAGGAAGACGAACGTCTGCGCGCAGACGAGGACG

LeuTrpMetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsnLeuValIleLeu  
1861 TTGTGGATGATGCTACTCATATCCCAAGCGGAGGCGGCTTTGGAGAACCTCGTAATACTT  
AACACCTACTACGATGAGTATAGGGTTCGCTCCGCCGAACCTCTTGAGCATTATGAA

AsnAlaAlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuValPhePheCysPhe  
1921 AATGCAGCATCCCTGGCGGGACGCACGGTCTTGATCCTTCCTCGTGTCTTCTGCTTT  
TTACGTCGTAGGGACCGGCCCTGCGTCCAGAACATAGGAAGGAGCACAAGAACGAA

AlaTrpTyrLeuLysGlyLysTrpValProGlyAlaValTyrThrPheTyrGlyMetTrp  
1981 GCATGGTATTTGAAGGGTAAGTGGGTGCCCGGAGCGGTCTACACCTTCTACGGGATGTGG  
CGTACCATAAACTTCCCATTCACCCACGGGCTCGCCAGATGTGGAAGATGCCCTACACC

ProLeuLeuLeuLeuLeuAlaLeuProGlnArgAlaTyrAlaLeuAspThrGluVal  
2041 CCTCTCCTCCTGCTCCTGTTGGCGTTGCCCGAGCGGCGTACGCGCTGGACACGGAGGTG  
GGAGAGGAGGACGAGGACAACCGCAACGCGGCTCGCCGCGATGCGCGACCTGTGCCCTCAC

AlaAlaSerCysGlyGlyValValLeuValGlyLeuMetAlaLeuThrLeuSerProTyr  
2101 GCCGCGTCGTGTGGCGGTGTTGTTCTCGTGGGTTGATGGCGCTGACTCTGTACCATAT  
CGGCGCAGCACACCGCCACAACAAGAGCAGCCCACTACCGCGACTGAGACAGTGGTATA

TyrLysArgTyrIleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeuThrArgValGlu  
2161 TACAAGCGCTATATCAGCTGGTGTGTGGTGGCTTCAGTATTTCTGACCAGAGTGGAA  
ATGTTTCGCGATATAGTCGACCACGAACACCACCGAAGTCATAAAAGACTGGTCTCACCTT

AlaGlnLeuHisValTrpIleProProLeuAsnValArgGlyGlyArgAspAlaValIle  
2221 GCGCAACTGCACGTGTGGATTCCCCCTCAACGTCCGAGGGGGGCGCGACGCGCTCATC  
CGCGTTGACGTGCACACCTAAGGGGGGAGTTGCAGGCTCCCCCGCGCTGCGGCAGTAG

LeuLeuMetCysAlaValHisProThrLeuValPheAspIleThrLysLeuLeuLeuAla  
2281 TTAATCATGTGTGCTGTACACCGACTCTGGTATTTGACATCACCAGATTGCTGCTGGCC  
AATGAGTACACAGCATGTGGGCTGAGACCATAAACTGTAGTGTTTAACGACGACCGG

ValPheGlyProLeuTrpIleLeuGlnAlaSerLeuLeuLysValProTyrPheValArg  
2341 GTCTTCGGACCCCTTTGGATTCTTCAAGCCAGTTTGCTTAAAGTACCCTACTTTGTGCGC  
CAGAAGCCTGGGGAACCTAAGAAGTTCGGTCAAACGAATTTTCATGGGATGAACACGCG

ValGlnGlyLeuLeuArgPheCysAlaLeuAlaArgLysMetIleGlyGlyHisTyrVal  
2401 GTCCAAGGCCTTCTCCGTTCTGCGGTTAGCGCGGAAGATGATCGGAGGCCATTACGTG  
CAGGTTCCGGAAGAGGCCAAGACGCGCAATCGCGCTTCTACTAGCCTCCGGTAATGCAC

GlnMetValIleIleLysLeuGlyAlaLeuThrGlyThrTyrValTyrAsnHisLeuThr  
2461 CAAATGGTCATCATTAAAGTTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCACT  
GTTTACCAGTAGTAATTCATCCCGCGAATGACCGTGGATACAAATATTGGTAGAGTGA

ProLeuArgAspTrpAlaHisAsnGlyLeuArgAspLeuAlaValAlaValGluProVal  
2521 CCTCTTCGGGACTGGGCGCACACCGCTTGGAGATCTGGCCGTGGCTGTAGAGCCAGTC  
GGAGAAGCCCTGACCCGCGTGTGGCGAACGCTCTAGACCGGACCGACATCTCGGTGAG

ValPheSerGlnMetGluThrLysLeuIleThrTrpGlyAlaAspThrAlaAlaCysGly  
2581 GTCTTCTCCAAATGGAGACCAAGCTCATACGTGGGGGGCAGATACCGCCGCGTGGCGT  
CAGAAGAGGGTTTACCTCTGGTTCGAGTAGTGCACCCCGCTATGGCGGCGCACGCGCA

AspIleIleAsnGlyLeuProValSerAlaArgArgGlyArgGluIleLeuLeuGlyPro  
2641 GACATCATCAACGGCTTGCCTGTTCCGCCGCGAGGGGCGGAGATACTGCTCGGGCCA  
CTGTAGTAGTTGCCGAACGGACAAGGGGCGTCCCGGCCCTCTATGACGAGCCCGGT



FIG. 54D

2701 AlaAspGlyMetValSerLysGlyTrpArgLeuLeuAlaProIleThrAlaTyrAlaGln  
GCCGATGGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCCATCACGGCGTACGCCCAG  
CGGCTACCTTACCAGAGGTTCCCCACCTCCAACGACCGGGGTAGTGGCGCATGCGGGTC

2761 GlnThrArgGlyLeuLeuGlyCysIleIleThrSerLeuThrGlyArgAspLysAsnGln  
CAGACAAGGGGCTCCTAGGGTGCATAATCACCAGCCTAACTGGCCGGGACAAAAACCAA  
GTCTGTTCCCCGGAGGATCCACGTATTAGTGGTCGGATTGACCGGCCCTGTTTTTGGTT

2821 ValGluGlyGluValGlnIleValSerThrAlaAlaGlnThrPheLeuAlaThrCysIle  
GTGGAGGGTGAGGTCCAGATTGTGTCAACTGCTGCCAAACCTTCTGGCAACGTGCATC  
CACCTCCCACTCCAGGTCTAACACAGTTGACGACGGGTTTGAAGGACCGTTGCACGTAG

2881 AsnGlyValCysTrpThrValTyrHisGlyAlaGlyThrArgThrIleAlaSerProLys  
AATGGGGTGTGCTGGACTGTCTACCAGGGGCGGAACGAGGACCATCGCGTCACCCAAG  
TTACCCACACGACCTGACAGATGGTGCCCGGCCCTTGCTCCTGGTAGCGCAGTGGGTTCT

2941 GlyProValIleGlnMetTyrThrAsnValAspGlnAspLeuValGlyTrpProAlaPro  
GGTCTGTCTATCCAGATGTATACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCCG  
CCAGGACAAGTAGGTTACATATGTTACATCTGGTTCTGGAACACCCGACCGGGCGAGGC

3001 GlnGlySerArgSerLeuThrProCysThrCysGlySerSerAspLeuTyrLeuValThr  
CAAGGTAGCCGCTCATTGACACCTGCACTTGCGGCTCCTCGGACCTTTACCTGGTCACG  
GTTCCATCGGCGAGTAACTGTGGGACGTGAACGCCGAGGAGCCTGGAATGGACCAAGTC

3061 ArgHisAlaAspValIleProValArgArgArgGlyAspSerArgGlySerLeuLeuSer  
AGGCACGCCGATGTCTATCCCGTGCGCCGGGCGGGGTGATAGCAGGGGCGAGCTGTGTCTG  
TCCGTGCGGCTACAGTAAGGGGACGCGGCCGCCCCACTATCTGTCCTCGGACGACAGC

3121 ProArgProIleSerTyrLeuLysGlySerSerGlyGlyProLeuLeuCysProAlaGly  
CCCCGGCCATTTCTACTTGAAAGGCTCCTCGGGGGGTCCGCTGTTGTGCCCGCGGGG  
GGGGCCGGGTAAAGGATGAACCTTCCGAGGAGCCCCCAGGCGACAACAGGGGCGCCCC

3181 HisAlaValGlyIlePheArgAlaAlaValCysThrArgGlyValAlaLysAlaValAsp  
CACGCCGTGGGCATATTTAGGGCGCGGTGTGCACCCGTGGAGTGGCTAAGGCGGTGGAC  
GTGCGGCACCCGTATAAATCCCGGCGCCACACGTGGGCACCTACCGATTCCGCCACCTG

3241 PheIleProValGluAsnLeuGluThrThrMetArgSerProValPheThrAspAsnSer  
TTTATCCCTGTGGAGAACCTAGAGACAACCATGAGGTCCCCGGTGTTCACGGATAACTCC  
AAATAGGGACACCTCTTGATCTCTGTTGGTACTCCAGGGGCCACAAGTGCTATTGAGG

3301 SerProProValValProGlnSerPheGlnValAlaHisLeuHisAlaProThrGlySer  
TCTCCACCAAGTAGTGCCCCAGAGCTTCCAGGTGGCTCACCTCCATGCTCCACAGGCAGC  
AGAGGTGGTCATCACGGGGTCTCGAAGGTCCACCGAGTGGAGGTACGAGGGTGTCCGTCG

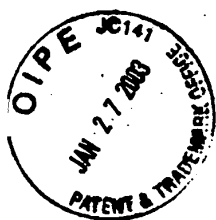
3361 GlyLysSerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeu  
GGCAAAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTC  
CCGTTTTCTGTTGTTCCAGGGCCGACGTATACGTGAGTCCCGATATTCCACGATCATGAG

3421 AsnProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIle  
AACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATC  
TTGGGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAG

3481 AspProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSer  
GATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCC  
CTAGGATTGTAGTCTGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGG

3541 ThrTyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIle  
ACCTACGGCAAGTTCTTGGCGACGGCGGGGTGCTCGGGGGGCGCTTATGACATAATAATT  
TGGATGCCGTTCAAGGAACGGCTGCCGCCACGAGCCCCCGCAATACTGTATTATTAA

3601 CysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAsp  
TGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCGGCACTGTCTTGAC  
ACACTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAGCCGTGACAGGAAGTC



# FIG. 54E

3661 GlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySer  
CAAGCAGAGACTGCGGGGCGAGACTG6TTGTGCTCGCCACCGCCACCCCTCCGGGCTCC  
GTTCTGTCTCTGACGCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCGAGG

3721 ValThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIlePro  
GTCACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCT  
CAGTGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGA

3781 PheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCys  
TTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGAGACATCTCATCTTCTGT  
AAAATGCCGTTCCGATAGGGGGAGCTTCATTAGTCCCCCCTCTGTAGAGTAGAAGACA

3841 HisSerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAla  
CATTCAAAGAAGAAGTGCGACGAACCTCGCCGCAAAGCTGGTCGATTGGGCATCAATGCC  
GTAAGTTTCTTCTTACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGG

3901 ValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValVal  
GTGGCCTACTACCGCGGTCTTGACGTGTCCGTCTATCCGACCAGCGGCGATGTTGTCTGT  
CACCGGATGATGGCGCCAGAAGTGCACAGGCAAGTAGGGCTGGTGGCCGCTACAACAGCAG

3961 ValAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCys  
GTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGC  
CACCGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACG

4021 AsnThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThr  
AATACGTGTGTACCCAGACAGTCGATTTACGCTTGACCCTACCTTACCATTGAGACA  
TTATGCACACAGTGGGTCTGTCAAGTAAAGTCGGAAGTGGGATGGAAGTGGTAACCTGT

4081 IleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGly  
ATCAGCTCCCCAGGATGCTGTCTCCGCACTCAACGTGCGGGCAGGACTGGCAGGGGG  
TAGTGCGAGGGGGTCTACGACAGAGGGCGTGAGTTGACGCCCGTCTGACCGTCCCC

4141 LysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSer  
AAGCCAGGCATCTACAGATTTGTGGCACCAGGGGAGCGCCCTCCGGCTGTTCCGACTCG  
TTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGC

4201 SerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGlu  
TCCGTCTCTGTGAGTGCTATGACGACGGCTGTGCTTGGTATGAGCTCACGCCCGGAG  
AGGACAGGAGACTCACGATACTGCGTCCGACACGAACATACTCGAGTGCGGGCGGCTC

4261 ThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHis  
ACTACAGTTAGGCTACGAGCGTACATGAACACCCGGGGCTTCCGCTGTGCCAGGACCAT  
TGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACAGGTCTCTGGA

4321 LeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSer  
CTTGAATTTTGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCC  
GAACTTAAACCCCTCCGCGAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGG

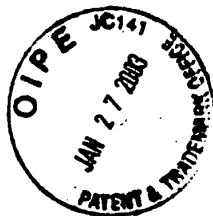
4381 GlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCys  
CAGACAAAGCAGAGTGGGGAGAACCTTCTTACCTGGTAGCGTACCAAGCCACCGTGTGC  
GTCTGTTTCTCTCACCCCTCTTGAAGGAATGGACCATCGCATGGTTCGGTGGCACACG

4441 AlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeu  
GCTAGGGCTCAAGCCCCTCCCCATCGTGGGACCAAGATGTGGAAGTGTGTTGATTGCGCTC  
CGATCCCGAGTTCGGGGAGGGGGTAGCACCTGGTCTACACCTTCAAACTAAGCGGAG

4501 LysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGlu  
AAGCCACCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTGAGAAAGAA  
TTCGGGTGGGAGGTACCGGTTGTGGGGACGATATGCTGACCCGCGACAAGTCTTACTT

4561 IleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGlu  
ATCACCTGACGCACCCAGTACCAAATACATCATGACATGATGTGCGCCGACCTGGAG  
TAGTGGGACTGCGTGGGTAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCTC

4621 ValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCys  
GTCGTACGAGCACCTGGGTGCTCGTTGGCGGCGTCTGGCTGCTTTGGCCGCGTATTGC  
CAGCAGTGCTCGTGGACCCACGAGCAACCGCCGAGGACCGACGAAACCGGCGCATAACG



# FIG. 54F

LeuSerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIle  
4681 CTGTCAACAGGCTGCGTGGTCATAGTGGGACAGGCTCGTCTTGTCCGGGAAGCCGGCAATC  
GACAGTTGTCCGACGCACCAAGTATCACCCGTCCAGCAGAACAGGCCCTTCGGCCGTTAG

IleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHis  
4741 ATACCTGACAGGGAAGTCTCTACCGAGAGTTCGATGAGATGGAAGAGTGTCTCAGCAC  
TATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTACGAGAGTCTGTG

LeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGly  
4801 TTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGC  
AATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCG

LeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAspTrp  
4861 CTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGG  
GAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACC

GlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPhelIleSerGlyIleGlnTyr  
4921 CAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACCTTCATCAGTGGGATACAATAC  
GTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCATGTTATG

LeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThr  
4981 TTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACA  
AACCGCCCGAACAGTTGCGACGGACCATTTGGGGCGGTAACGAAGTAACACGAAAATGT

AlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGly  
5041 GCTGCTGTCAACAGCCCACTAACCCTAGCCAAACCTCCTCTTCAACATATTGGGGGGG  
CGACGACAGTGGTGGGTGATTGGTGATCGGTTGGGAGGAGAAGTTGTATAACCCCCC

TrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeu  
5101 TGGGTGGCTGCCAGCTCGCCGCCCGGTCGCGCTACTGCCTTTGTGGGCGCTGGCTTA  
ACCCACCGACGGGTCGAGCGGGCGGGGCCACGGCGATGACGGAACACCCGCGACCGAAT

AlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGly  
5161 GCTGGCGCCGCCATCGGCAGTGTGGACTGGGGAAGGTCTCATAGACATCCTTGCAGGG  
CGACCGCGGGTAGCCGTCAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCC

TyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValPro  
5221 TATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCC  
ATACCGCGCCCGACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCATCCAGGGG

SerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValVal  
5281 TCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTC  
AGGTGCCTCCTGGACCAAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAG

GlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGln  
5341 GGCCTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGCGAGTGCAG  
CCGACCAAGACAGTCTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCGTCACGTC

TrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyr  
5401 TGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGAACCATGTTTCCCCACGCACTAC  
ACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGGTGATG

ValProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThr  
5461 GTGCCGGAGAGCGATGCAGCTGCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACC  
CACGGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTGGAGTGACATTGG

GlnLeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGly  
5521 CAGCTCCTGAGGCGACTGCACCAAGTGGATAAGCTCGGAAGTGTACCACTCCATGCTCCGGT  
GTCGAGGACTCCGCTGACGTGGTCACTATTGAGCCTCACATGGTGAGGTACGAGGCCA

SerTrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrp  
5581 TCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGG  
AGGACCGATTCCCTGTAGACCTGACCTATACGCTCCACAACCTCGCTGAAATTCTGGACC

LeuLysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGly  
5641 CTAAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCTTTGTGTCTGCCAGCGCGGG  
GATTTTCGATTGAGTACGGTGTGACGCGACCTAGGGGAAACACAGGACGGTGCAGCCC



# FIG. 54G

5701 TyrLysGlyValTrpArgValAspGlyIleMethHisThrArgCysHisCysGlyAlaGlu  
TATAAGGGGGTCTGGCGAGTGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAG  
ATATTCCTCCAGACCGCTCACCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTC

5761 IleThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsn  
ATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCTAGGACCTGCAGGAAC  
TAGTGACCTGTACAGTTTTTGCCTGCTACTCTAGCAGCCAGGATCCTGGACGTCTTG

5821 MetTrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuPro  
ATGTGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCTGTACCCCCCTTCCT  
TACACCTCACCTGGAAGGGGTAATTACGGATGTGGTGCCGGGGACATGGGGGGAAGGA

5881 AlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArg  
GCGCCGAACCTACACGTTGCGCTATGGAGGGTGTCTGCAGAGGAATATGTGGAGATAAGG  
CGCGGCTTGATGTGCAAGCGCATACCTCCACAGACGTCTCTTATACACCTCTATTCC

5941 GlnValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCys  
CAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTCAAATGCCCGTGC  
GTCCACCCCTGAAGGTGATGCACTGCCATACTGATGACTGTTAGAGTTTACGGGACG

6001 GlnValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAla  
CAGGTCCCATCGCCGAATTTTTACAGAATTGGACGGGGTGCCTACATAGGTTTGCG  
GTCCAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGC

6061 ProProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyr  
CCCCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTGAGAGTAGGACTCCACGAATAC  
GGGGGGACGTTGCGGAACGACGCCCTCTCCATAGTAAGTCTCATCTGAGGTGCTTATG

6121 ProValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMet  
CCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCGTGTGACGTCCATG  
GGCCATCCAGCGTTAATGGAACGCTCGGGCTTGCCCTGCACCGGCACAACCTGCAGGTAC

6181 LeuThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySer  
CTCACTGATCCCTCCCATATAACAGCAGAGGCGGGCGGGCGAAGGTTGGCGAGGGGATCA  
GAGTGACTAGGGAGGGTATATTGTCGTCTCCGCGGGCCGCTTCCAACCGCTCCCCTAGT

6241 ProProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThr  
CCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACT  
GGGGGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGA

6301 CysThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArg  
TGACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCAACCTCTATGGAGG  
ACGTGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCC

6361 GlnGluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAsp  
CAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGAC  
GTCTCTACCCGCCGTTGTAGTGGTCCCAACTAGTCTTTTGTTCACCACTAAGACCTG

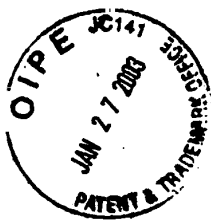
6421 SerPheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIle  
TCCTTCGATCCGCTTGTGGCGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATC  
AGGAAGCTAGGCGAACACCGCTCCTCTGCTCGCCCTCTAGAGGATGGGCGTCTTTAG

6481 LeuArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsn  
CTGCGGAAGTCTCGGAGATTGCCCCAGGCCCTGCCGTTTGGGCGCGCCGGACTATAAC  
GACGCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAACCCGCGCCGGCCTGATATTG

6541 ProProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCys  
CCCCGCTAGTGGAGAGCTGGAAGGAGCCGACTACGAACCACTGTGGTCCATGGCTGT  
GGGGGCGATCACCTCTGACCTTTTTTGGGCTGATGCTTGGTGACACCAAGGTACCGACA

6601 ProLeuProProProLysSerProProValProProProArgLysLysArgThrValVal  
CCGCTTCCACCTCAAAGTCCCCTCCTGCTCCGCTCGGAAGAAGCGGACGGTGGTC  
GGCGAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCTGCCACCAAG

6661 LeuThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySer  
CTCACTGAATCAACCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGC  
GAGTGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCAAAACCGTGC



# FIG. 54H

6721 SerSerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSer  
TCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCCCCTTCT  
AGGAGTTGAAGGCCGTAATGCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAGA

6781 GlyCysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGlu  
GGCTGCCCCCGACTCCGACGCTGAGTCTTCTCCATGCCCCCTGGAGGGGGAG  
CCGACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTC

6841 ProGlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAla  
CCTGGGGATCCGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCAACGCG  
GGACCCCTAGGCTAGAATCGCTGCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGC

6901 GluAspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCys  
GAGGATGTCGTGCTGCTCAATGCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGC  
CTCCTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCAGC

6961 AlaAlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHis  
GCCGCGAAGAACAGAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCAACAC  
CGGCGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTGCTTGAGCAACGATGCAGTGGTG

7021 AsnLeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPhe  
AATTTGGTGTATTCCACCACCTCAGCAGTGTGCTGCAAAAGGCAAGAAAGTCACATTT  
TTAAACACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTA

7081 AspArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAla  
GACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCG  
CTGTCTGACGTTCAAGACCTGTGCGTAATGGTCTGCATGAGTTCTCCAATTCGTGCGC

7141 AlaSerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProPro  
GCGTCAAAAGTGAAGGCTAAGTTGCTATCCGTAGAGGAAGCTTGCAACCTGACGCCCCCA  
CGCAGTTTTCACTCCGATTGAACGATAGGCATCTCCTCGAACGTCGGACTGCGGGGGT

7201 HisSerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLys  
CACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTTCCGTTGCCATGCCAGAAAG  
GTGAGTGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTC

7261 AlaValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIle  
GCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAAACCAATA  
CGGCATTGGGTGATGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTAT

7321 AspThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArg  
GACACTACCATCATGGCTAAGAACGAGTTTTCTGCGTTTCAGCCTGAGAGGGGGGTCGT  
CTGTGATGGTAGTACCGATTCTTGTCTCAAAAGACGCAAGTCGGACTCTTCCCCCAAGCA

7381 LysProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAla  
AAGCCAGCTCGTCTCATCGTGTCCCCGATCTGGGCGTGCAGCTGTGCGAAAGATGGCT  
TTCGGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGA

7441 LeuTyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGln  
TTGTACGACGTGGTTACAAAGCTCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAA  
AACATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTT

7501 TyrSerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrPro  
TACTCACCAGGACAGCGGTTGAATTCCTCGTCAAGCGTGGAAGTCCAAGAAAACCCCA  
ATGAGTGGTCTGTGCCCCAATTAAGGAGCACGTTCCACCTTCAGGTTCTTTTGGGGT

7561 MetGlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArg  
ATGGGGTTCTCGTATGATACCCGCTGCTTGAAGTCCACAGTCACTGAGAGCGACATCCGT  
TACCCCAAGAGCATACTATGGGCGACGAACTGAGGTGTCACTGACTCTCGCTGTAGGCA

7621 ThrGluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLys  
ACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCAAGCCCGCTGGCCATCAAG  
TGCTCCTCCGTAGATGGTTACAACACTGGAGCTGGGGGTTGGGGCGCACCGGTAGTTC

7681 SerLeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCys  
TCCCTCACCAGAGAGGCTTTATGTTGGGGGCCCTTACCAATTCAAGGGGGGAGAACTGC  
AGGGAGTGGCTCTCCGAAATACAACCCCGGGAGAATGGTTAAGTTCCCCCTCTTGACG



## FIG. 54I

7741 GlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThr  
GGCTATCGCAGGTGCCGCGCGAGCGGCGTACTGACAAGTACTGTGGTAACACCCTCACT  
CCGATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGA

7801 CysTyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeu  
TGCTACATCAAGGCCCGGGCAGCCTGTGAGCCGAGGGCTCCAGGACTGCACCATGCTC  
ACGATGTAGTTCGGGGCCGTCGGACAGCTCGGCGTCCGAGGTCCTGACGTGGTACGAG

7861 ValCysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAla  
GTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGCG  
CACACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGC

7921 SerLeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProPro  
AGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCTGGGGACCCCCCA  
TCGGACTCTCGGAAGTGCTCCGATACTGGTCCATGAGGCGGGGGGACCCCTGGGGGGT

7981 GlnProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHis  
CAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTGAGTCGCCCAC  
GTTGGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTG

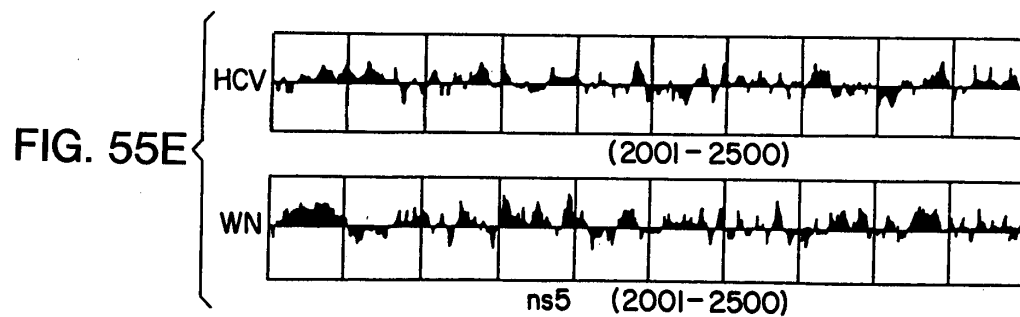
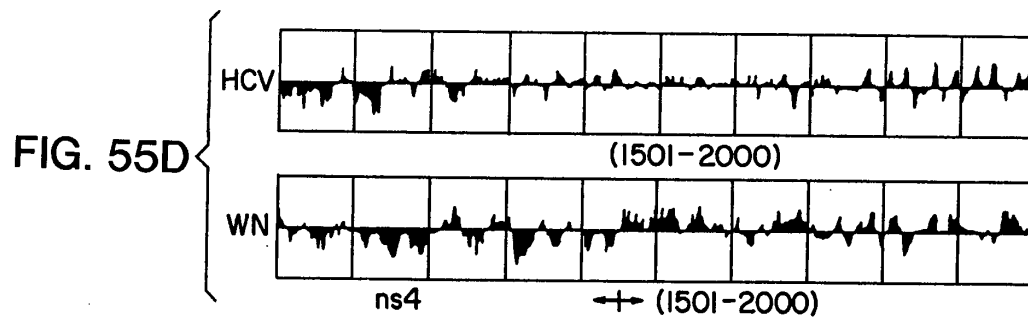
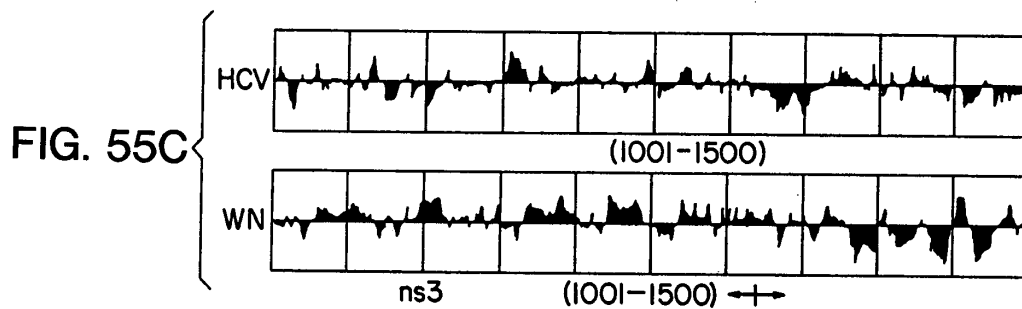
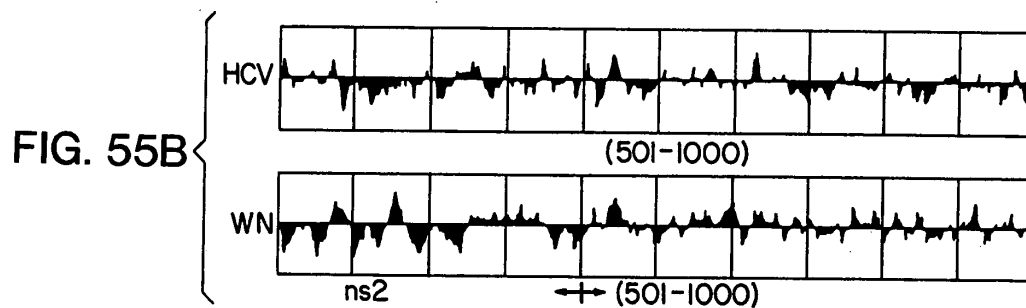
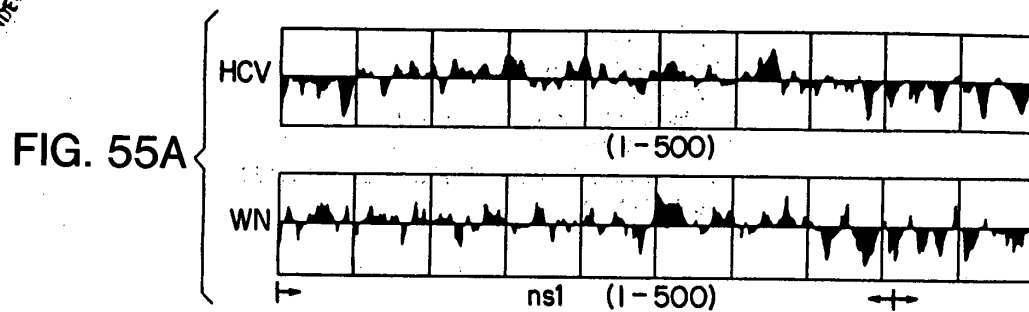
8041 AspGlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArg  
GACGGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGA  
CTGCCGCGACCTTCTCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGCTCT

8101 AlaAlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMet  
GCTGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATG  
CGACGCACCCCTCTGTCGTTCTGTGTGAGGTGAGTTAAGGACCGATCCGTTGTATTAGTAC

8161 PheAlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIle  
TTTGCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATA  
AAACGGGGGTGTGACACCCGCTCTACTATGACTACTGGGTAAAGAAATCGCAGGAATAT

8221 AlaArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIle  
GCCAGGGACAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATA  
CGGTCCCTGGTCGAACCTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTAT

8281 GluProLeuAspLeuProProIleIleGlnArgLeu  
GAACCACTTGATCTACCTCCAATCATTCAAAGACTC  
CTTGGTGAAGTAGATGGAGGTTAGTAAGTTTCTGAG





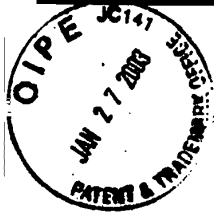


FIG. 56

ArgArgSerArgAsnLeuGlyLysValIleAspThrLeuThrCysGlyPheAlaAsp  
1 CCCGGCGTAGGTCGCGCAATTGGGTAAGGTACATACCTTACGTGCGGCTTCGCCG  
GGCCGCATCCAGCGCGTTAAACCCATTCCAGTAGCTATGGGAATGCACGCCGAAGCGGC  
LeuMetGlyTyrIleProLeuValGlyAlaProLeuGlyGlyAlaAlaArgAlaLeuAla  
61 ACCTCATGGGTACATACCGCTCGTCGGCGCCCTCTTGGAGCGCTGCCAGGCCCTGG  
TGGAGTACCCCATGTATGGCGAGCAGCCGCGGGAGAACCTCCGCGACGGTCCCGGACC  
HisGlyValArgValLeuGluAspGlyValAsnTyrAlaThrGlyAsnLeuProGlyCys  
121 CGCATGGCGTCGGGTTCTGGAAGACGGCGTGAACATATGCAACAGGAACCTTCCTGGTT  
GGTACCGCAGGCCCAAGACCTTCTGCCGCACTGATACGTTGTCTTGGAAAGACCAA  
SerPheSerIlePheLeuLeuAlaLeuLeuSerCysLeuThrValProAlaSerAlaTyr  
181 GCTCTTCTCTATCTTCTTGGCCCTGCTCTCTGCTTGACTGTGCCCGCTTCGGCCT  
CGAGAAAGAGATAGAGGAAGACCGGACGAGAGAACGAACCTGACACGGCGGAAGCCGA  
-----  
GlnValArgAsnSerThrGlyLeuTyrHisValThrAsnAspCysProAsnSerSerIle  
241 ACCAAGTGCGCAACTCCACGGGCTTTACCACGTCACCAATGATTGCCCTAACCTCGAGTA  
TGGTTCACGCGTTGAGGTGCCCCGAAATGGTGCACTGTTACTAACGGGATTGAGCTCAT  
-----overlap with CA167b-----  
ValTyrGluAlaAlaAspAlaIleLeuHisThrProGlyCysValProCysValArgGlu  
301 TTGTGTACGAAGCGCGATGCCATCCTGCACACTCCGGGGTGGTCCCTTGGCTTCGTG  
AACACATGCTTCGCCGCTACGGTAGGACGTGTGAGGCCCCCACGACGGAACGCAAGCAC  
-----  
GlyAsnAlaSerArgCysTrpValAlaMetThrProThrValAla  
361 AGGCCAACGCCCTCGAGGTGTTGGGTGGCGATGACCCCTACGGTGGCC  
TCCCGTTGCGGAGCTCCACAACCCACCGCTACTGGGGATGCCACCCG



LysLysAsnLysArgAsnThrAsnArgArgProGlnAspValLysPheProGlyGlyGly  
1 AAAAAAACAACGTAACACACCGTCGCCACAGGACGTCAAGTCCCGGGTGGCG  
TTTTTTTTTTGTTGCAATGTGTTGGCAGCGGTGTCTCGAGTTCAAGGCCCCACCGC  
GlnIleValGlyValTyrLeuLeuProArgArgGlyProArgLeuGlyValArgAla  
61 GTCAGATCGTTGGTGGAGTTACTTGTTCGCCGCGAGGGCCCTAGATTGGTGTGGCG  
CAGCTAGCAACCACTCAATGAACAACGGCGTCCCCGGGATCTAACCCACACGCGC  
ThrArgLysThrSerGluArgSerGlnProArgGlyArgGlnProIleProLysAla  
121 CGACGAGAAAGACTTCGAGCGGTGCAACCTCGAGGTAGACGCCAGCTATCCCCAAG  
GCTGCTCTTCTGAAGCTCGCCAGCGTTGGAGCTCCATCTCGGTCCGATAGGGGTTC  
ArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpProLeuTyrGlyAsn  
181 CTCGTCGGCCCCAGGAGGAGACTGGGCTCAGCCCGGTACCTTGGCCCCCTCTATGGCA  
GAGCAGCCGGGCTCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGGAGATACCGT  
GluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArgProSerTrpGly  
241 ATGAGGGCTGCGGTGGCGGATGGCTCTGTCTCCCCGTGGCTCTCGGCCTAGCTGG  
TACTCCCGACGCCCAACCGCCCTACCGAGGACAGAGGGCACCGAGCCGGATCGACCC  
-----  
ProThrAspProArgArgArgSerArgAsnLeuGlyLysValIleAspThrLeuThrCys  
301 GCCCCACAGACCCCGCGTAGGTGCGGCAATTGGGTAAGGTCAATCGATACCCCTTACGT  
CGGGGTGTCTGGGGCCGCATCCAGCGGTTAAACCCATTCCAGTAGCTATGGGAATGCA  
-----  
GlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeuGlyGlyAlaAla  
361 GCGGCTTCGCCGACCTCATGGGTACATACCGCTCGTCGGCGCCCTCTTGGAGCGCTG  
CGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGCCGCGGGGAGAACCTCCCGGAC  
-----  
ArgAlaLeuAlaHisGlyValArgValLeuGluAspGlyValAsnTyrAlaThrGlyAsn  
421 CCAGGGCCCTGGCGCATGGCTCCGGTTCTGGAAGACGCGCTGAACATGCAACAGGGA  
GGTCCCCGGACCGGTACCGCAGGCCCAAGACCTTCTGCCGCACTTGATACGTTGTCCCT  
-----  
LeuProGlyCysSerPheSerThrPhe  
481 ACCTTCTCTGGTTGCTCTTTCTCTACCTTC  
TGGAAGGACCAACGAGAAAGAGATGGAAG

FIG. 57

# FIG. 58A

#MetSerValValGlnProProGlyProProLeu

1 CGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTCAGCCCTCCAGAGACCCCCC  
#MetAlaLeuValOP

GCGTCTTTCCGAGATCGGTACCCGCAATCATACTCACAGCAGGTCCGAGGTCCCTGGGGGGG

ProGlyGluProAM

61 TCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGAC  
AGGGCCCTCTCGGTATCACAGACGCCCTTGCCACTCATGTGCCCTTAACGGTCCCTGCTG

#MetProGlyAspLeuGlyValProProGlnAsp

121 CGGCTCCTTTCTTGGATCAACCCGCTCAATGCCCTGAGATTGGCGTGCCCCCGCAAGA  
GCCCAGGAAGAACCCTAGTTGGCGAGTTACGGAACCTCTAACCAGGCGGCGTTCT

CysAM

OP AM GlyAlaCys  
\*

181 CTGCTAGCCGAGTAGTGTGGGTCCGAAAGCCCTTGTGCTACTGCCCTGATAGGGTGCTT  
GACGATCGGCTCATCACAAACCCAGCGCTTCCGGAACACCATGACGACTATCCACGAA

GluCysProGlyArgSerArgArgProCysThrMetSerThrAsnProLysProGlnLys



FIG. 58B

241

GGGAGTCCCCGGGAGGTCTCGTAGACCGTGCCACCATGAGCAGCAATCCTAAACCTCAA  
CGCTCAGGGGGCCCTCCAGAGCATCTGGCACGTGGTACTCGTCTTAGGATTGGAGTTT

LysAsnLysArgAsnThrAsnArgArgProGlnAspValLysPheProGlyGlyGln

301

AAAAAACAACGTAACACCAACCGTCGCCACAGACGTCAGTCCCGGGTGCGGTC  
TTTTTTTGTTCATTGTGTTGGCAGCGGGTGTCCTGCAGTTCAAGGGCCACCGCCAG

IleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeuGlyValArgAlaThr

361

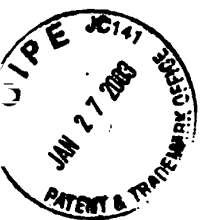
AGATCGTTGCTGAGCTTACTTGTGTCGCCGAGGGGCCCTAGATTGGGTGCGCGGA  
TCTAGCAACCACTCAAATGAACAACGGCGGTCCCCGGGATCTAACCACACGCGCGCT

ArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnProIleProLysAlaArg

421

CGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCTATCCCCAAGGCTC  
GCTCTTTCTGAAGGCTCGCCAGCGTTGAGCTCCATCTGCAGTCGGATAGGGGTTCCGAG

ArgProGluGlyArgThrTrpAlaGlnProGlyTyrProThrProLeuTyrGlyAsnGlu



481 -----overlap with CA290a-----  
 GTGCGCCGAGGCGCAGACCTGGCTCAGCCCGGTACCTTGCCCTATGGCAATG  
 CAGCCGGGCTCCCGTCCCTGACCCGAGTCGGGCCCATGGGAACCGGGAGATACCGTTAC

GlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArgProSerTrpGlyPro

541 -----  
 AGGCTGCGGGTGGGGGATGCTCCTGCTCTCCCGTGCTCTGGCCTAGCTGGGCC  
 TCCCGACGCCACCCGCCCTACCGAGACAGAGGGGCACCGAGCCGGATCGACCCCGG

ThrAspProArgArgSerArgAsnLeuGlyLysValIleAspThrLeuThrCysGly

601 -----  
 CCACAGACCCCGCGGTAGTCCGCCAATTGGGTAAGCTCATCGATACCTTACGTGCG  
 GGTGCTGGGGGCCCATCCAGCGCGTTAAACCATTCAGTAGCTATGGAAATGCACGC

Phe

661 -----  
 GCTTC  
 CGAAG

\* = Start of long HCV ORF  
 | = Putative first amino acid of large HCV polypeptide  
 # = Putative small encoded peptides (that may play a  
 translational regulatory role)

FIG. 58C

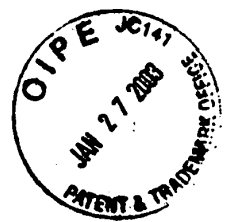


FIG. 59

1 ValLeuGIYArgGIUArgProCysGlyThraIaOP AM GlyAlaCysGluCysProGly  
GTCTTGGGTCGCGAAAGCCCTTGTTGGTACTGCTGATAGGGTGCTTGGAGTCCCCGGG  
CAGAACCAGCGCTTCCGGAACACCATGACGGACTATCCACGAACGCTCACGGGGCCC

\*

61 ArgSerARgArgProCysThrMetSerThraSnProLysProGlnArgLysThrLysArg  
AGGTCTCGTAGACCGCTGCACCATGAGCACGAATCCTAAACCTCAAGAAACCAACAGT  
TCCAGAGCATCTGGCACGTGGTACTCGTGTAGGATTTGGAGTTTCTTTTGGTTTCCA

121 AsnThrAsnArgArgProGlnAspValLysPheProGlyGlyGlyGlnIleValGlyGly  
AACACCAACCGTCGCCACAGACGTCAGATTCCCGGGTGGCGGTGAGATCGTTGGTGGA  
TTGTGGTTGGCAGCGGGTGTCTGCTGAGTTCAGGGGCCACCGCCAGTCTAGCAACCACT

181 ValTyrLeuLeuProArgArgGlyProArgLeuGlyValAlaArgAlaThrArgLysThrSer  
GTTTACTTGTGCCCCGCGCAGGGCCCTAGATTGGGTGTGCGCGCGACGAGAAAGACTTCC  
CAAATGAACAACGGCGCGCTCCCGGGAATTAACCCACACGCGCGCTGCTTTCTGAAGG

-----overlap with CA290a-----

241 GluArgSerGlnProArgGlyArgArgGlnProIleProLysAlaArgArgProGluGly  
GAGCGGTGCAACCTCGAGGTAGACGTCAGCCTATCCCAAGGCTGTCGGCCCCGAGGGC  
CTCGCCAGCGTTGAGCTCCATCTGCAGTCGGATAGGGGTTCCGAGCAGCCGGGCTCCCG

301 ArgThrTrpAlaGlnProGlyTyrProTrpProLeuTyrGlyAsnGluGlyCys  
AGGACCTGGGCTCAGCCCCGGGTACCTTGCCCCCTTATGGCAATGAGGGCTGCG  
TCCTGGACCCGAGTCGGGCCCATGGGAACCGGGGAGATACCGTTACTCCCGAGCGC

\* = putative initiator methionine codon

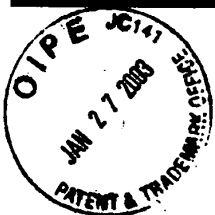


FIG. 60

```

#ProProop
#SerThrMetAsnHisSerProValArgAsnTyrCysLeuHisAlaGluSerValAM
1 #LeuHisHisGluSerLeuProCysGluGluLeuLeuSerSerArgArgLysArgLeuAla
CTCCACCATGATCATCCCTGTGAGGAATCTACTGCTTACGACGAAAGCGTCTAGCC
GAGGTGTTACTTAGTGAGGGGACACTCCTTGATGACACAGAAGTGCCTTTCCGAGATCGG
-----
#MetSerValValGlnProProGlyProProLeuProGlyGluProAM
MetAlaLeuValOP
61 ATGGCGTTAGTATGAGTGTCTGTCAGCCCTCCAGGACCCCTCCGGGAGAGCCATAGT
TACCGCAATCATACTCACACAGCAGCTCGAGGTCTCTGGGGGAGGCCCTCTCGGTATCA
-----
121 GGTCGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCTTCTTGATC
CCAGACGCCCTTGGCCACTCATGTGCCCTTAACGGTCTCTGGCCAGAAAGAACCTAG
-----
overlap with ag30a-----
#MetProGlyAspleuGlyValProProGlnAspCysAM
181 AACCCGCTCAATGCCCTGAGATTGGCGGTGCCCCGCAAGACTGCTAGCCGAGTAGTGT
TTGGCGAGTTACGGAACCTCTAAACCCGACGGGGCGTTCTGACGATCGGCTCATCACA
-----
241 TGGGTCGCGAAGGCCCTTGTGTTACTGCTGATAGGGT*GCGAGTGCCCCGGAGGT
ACCCAGCGCTTTCGGAACACCATGACGAGCTATCCACGAACGCTCACGGGGCCCTCCA
OP AM GlyAlaCysGluCysProGlyArgSer
-----
* = Start of long HCV ORF
# = Putative small encoded peptides (that may
play a translational regulatory role)
301 CTCGTAGA
GAGCATCT

```



FIG. 61

-----Overlap with 15e -----

1 GlyAlaCysTyrSerIleGluProLeuAspLeuProIleIleGlnArgLeuHisGly  
 1 GGGCCCTGCTACTCCATAGAACCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGC  
 CCCCAGACGATGAGGTATCTGTGTGACCTAGATGAGGTAGTAAAGTTTCTGAGGTACCG

LeuSerAlaPheSerLeuHisSerTyrSerProGlyGluIleAsnArgValAlaAlaCys  
 61 CTCAGCGCATTTTCACTCCACAGTTACTCTCCAGGTGAATTAATAGGCGGCCCATGC  
 GAGTCGCGTAAAGTGAGGTGTCAATGAGAGGTCCACTTTAATTATCCACCGCGGTACG

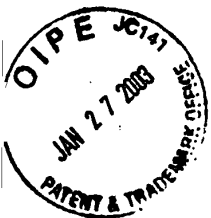
Gly\*  
 G

LeuArgLysLeuGlyValProProLeuArgAlaTrpArgHisArgAlaArgSerValArg  
 121 CTCAGAAACTTGGGGTACCGCCCTTGCGAGCTTGAGACACCGGGCCCGAGCGTCCGC  
 GAGTCTTTTGAAACCCCATGGCGGGAACGCTCGAACCTCTGTGGCCCGGCGCTCGCAGCGC

AlaArgLeuLeuAlaArgGlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrp  
 181 GCTAGGCTTCTGGCCAGAGAGGCGGCTGCCATATGTGCAAGTACCTCTTCAACTGG  
 CGATCCGAAGACCGGTCTCTCCGTCCCGACGGTATACACCGTTTCATGGAGAAGTTGACC

AlaValArgThrLysLeuLys  
 241 GCAGTAAGAACAAAGCTCAAAAC  
 CGTCATTTCTGTGTTCCGAGTTTG

\* = nucleotide heterogeneity





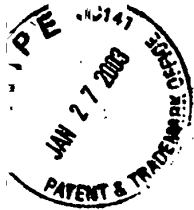


FIG. 62A

CACTCCACCATGAATCACTCCCCTGTGAGGAACTACTGTCTTCACGCAGAAAGCGTCTAG  
CCATGGCGTTAGTATGAGTGTCTGTCAGCCTCCAGGACCCCCCTCCCGGGAGAGCCATA  
GTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCTTTCTTGGA  
TCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCGCAAGACTGCTAGCCGAGTAGT  
GTTGGTGCAGAAAGGCCTTGTGGTACTGCCTGATAGGGTGTGCGAGTGCCCCGGGAG-300

---(Putative initiator methionine codon)

GTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACCTCAAAAAAAAAACAAACGTAA  
CACCAACCGTCGCCCACAGGACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGT  
TTACTTGTGGCGCGCAGGGGCCCTAGATTGGGTGTGCGCGCAGCAGAAAGACTTCCGA  
GCGGTGCGAACCTCGAGGTAGACGTACGCTATCCCCAAGGCTCGTCGGCCCGAGGGCAG  
GACCTGGGCTCAGCCCCGGGTACCCTTGGCCCCCTCTATGGCAATGAGGGTGCGGGTGGGC-600  
GGGATGGCTCCTGTCTCCCCGTGGCTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCG  
TAGGTGCGCAATTTGGGTAAAGGTATCGATACCCTTACGTGCGGCTTCGCCGACCTCAT  
GGGTACATACCGCTCGTCGGCGCCCCCTCTTGGAGGCGCTGCCAGGGCCCTGGCGCATGG  
CGTCCGGGTTCTGGAAGACGGCGTGAAGTATGCAACAGGGAACCTTCCTGGTTGCTCTTT  
CTCTATCTTCTTCTGGCCCTGCTCTCTTGTGCTGACTGTGCCCGCTTCGGCCTACCAAGT-900  
GCGCAACTCCACGGGGCTTTACCACGTACCAATGATTGCCCTAACTCGAGTATTGTGTA  
CGAGGCGGGCGATGCCATCTGACACTCCGGGGTGCCTCCCTTGCCTTGTGAGGGCAA  
CGCTCGAGGTGTTGGGTGGCGATGACCCCTACGGTGGCCACCAGGGATGGCAAACTCCC  
CGCGACGCAGCTTCGACGTACATCGATCTGCTTGTGCGGAGCGCCACCCTCTGTTCCGGC  
CCTCTACGTGGGGGACCTATGCGGGTCTGTCTTCTTGTGCGGCAACTGTTCACTTCTC-1200  
TCCACGGCGCACTGGACGACGCAAGGTTGCAATTGCTCTATCTATCCCGGCATATAAC  
GGGTACCGCATGGCATGGGATATGATGATGAAGTGGTCCCTACGACGGCTTGGTAAAT  
GGCTCAGCTGCTCCGGATCCCAAGCCATCTTGGACATGATCGCTGGTGTCTACTGGGG  
AGTCTTGGCGGGCATAGCGTATTTCTCCATGGTGGGGAACCTGGGCGAAGGTCTGGTAGT  
GCTGCTGCTATTTGCCGGCGTCGACGCGGAAACCCACGTACCGGGGGGAAGTGCCGGCCA-1500  
CACTGTGTCTGGATTTGTTAGCCTCTCGCACCAGGCGCAAGCAGACGTCCAGCTGAT  
CAACACCAACGGCAGTTGGCACCTCAATAGCACGGCCCTGAAGTGAATGATAGCTCAA  
CACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGTTCAACTCTTCAGGCTGTCTGA  
GAGGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACCAAGGCTGGGGCCCTATCAGTTA  
TGCCAACGGAAGCGGCCCGACGAGCGCCCTACTGCTGGCACTACCCCCAAAACCTTG-1800  
CGGTATTGTGCCCGCAAGAGTGTGTGTGGTCCGGTATATTGCTTCACTCCGACCCCGT  
GGTGGTGGGAACGACCGACAGGTGCGGCGCGCCACCTACAGCTGGGGTGAAGATGATAC  
GGACGTCTTCGTCTTAACAATACCAGGCCACCGCTGGGCAATTGGTTGGTTGTACCTG  
GATGAATCAACTGGATTACCAAAGTGTGCGGAGCGCCTCTTGTGTCATCGGAGGGGC  
GGGCAACACACCCTGCACTGCCCCACTGATTGCTCCGCAAGCATCCGGACGCCACATA-2100  
CTCTCAAGTGGGCTCCGGTCCCTGGATCACACCAGGTGCTTGGTGCAGTACCCGATAG  
GCTTTGGCATTATCCTTGTACCATCAACTACACCATATTTAAATCAGGATGTACGTGGG  
AGGGGTGGAACACAGGCTGGAAGCTGCCTGCAACTGGACGCGGGGCGAACGTTGCGATCT  
GGAAGACAGGGACAGGTCCGAGCTCAGCCGTTACTGCTGACCACTACACAGTGGCAGGT  
CCTCCCGTGTTCCTTCAACCCCTACCAGCCTTGTCCACCGGCCTCATCCACCTCCACCA-2400  
GAACATTGTGGACGTGCACTTGTACGGGGTGGGGTCAAGCATCGCGTCTGGGCCAT  
TAACTGGGAGTACGTCGTTCTCTGTTCTGCTTGCAGACGCGCGCTGCTCCTG  
CTTGTGGATGATGCTACTCATATCCCAAGCGGAGGCGGCTTGGAGAACCTCGTAATACT  
TAATGCAGCATCCCTGGCCGGGACGACGGTCTTGTATCCTTCTCGTGTCTTCTGCTT  
TGCATGGTATTTGAAGGGTAAGTGGGTGCCCGAGCGGTCTACACCTTCTACGGGATGTG-2700  
GCCTCTCCTCCTGCTCCTGTTGGCGTTGCCAGCGGGCGTACGCGCTGGACACGGAAGT  
GGCCGCGTCTGTGTCGGGTGTTGTTCTGCTCGGGTTGATGGCGCTGACTGTCAACATA  
TTACAAGCGCTATATCAGCTGGTGTGTTGGTGGCTTCAAGTATTTCTGACCAGAGTGG  
AGCGCAACTGCAGGTGTGGATTCCCCCCTCAACGTCCGAGGGGGGCGCGACGCCGTCTAT  
CTTACTCATGTGTGCTGTACACCGACTCTGGTATTTGACATACCAAATTGCTGTGTCG-3000  
CGTCTTGGACCCCTTTGGATTCTTCAAGCCAGTTTGTAAAGTACCCTACTTTGTGCG  
CGTCCAAGGCCTTCTCCGGTTCTGCGCGTTAGCGCGGAAGATGATCGGAGGCCATTACGT  
GCAAATGGTCATCATTAAAGTTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCAC  
TCCTCTTCCGGACTGGGCGCACAACGGCTTGGCAGATCTGGCCGTGGTGTAGAGCCAGT  
CGTCTTCTCCCAATGGAGACCAAGCTCATCAGTGGGGGGCAGATACCGCCGCGTGGCG-3300  
TGACATCATCAACGGCTTGCCTGTTTCCGCCGAGGGGCGGGAGATACTGCTCGGGCC  
AGCCGATGGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCCATCACGGCGTACGCCCA  
GCAGACAAGGGGCTCCTAGGGTGCATAATCACCAGCCTAACTGGCCGGGACAAAAACCA  
AGTGGAGGGTGAAGTCCAGATTGTGTCAACTGCTGCCCAACCTTCTGGCAACGTGCAT

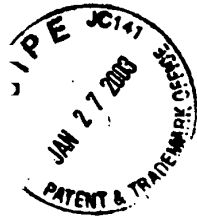


FIG. 62B

CAATGGGGTGTGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCATCGCGTCACCCAA-3600  
GGGTCTGTGCATCCAGATGTATACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCC  
GCAAGGTAGCCGCTCATTGACACCCTGCACTTGCGGCTCCTCGGACCTTTACCTGGTCAC  
GAGGCACGCCGATGTATTCCCGTGCGCCGGCGGGGTGATAGCAGGGGCAGCCTGCTGTC  
GCCCCGGCCCATTTCTACTTGAAAGGCTCCTCGGGGGGTCCGCTGTTGTGCCCGCGGG  
GCACGCCGTGGGCATATTTAGGGCCGCGGTGTGCACCCGTGGAGTGGCTAAGGCGGTGGA-3900  
CTTTATCCCTGTGGAGAACCTAGAGACAACCATGAGGTCCCCGGTGTTCACGGATAACTC  
CTCTCCACCAGTAGTGCCCCAGAGCTTCAGGTGGCTCACCTCCATGCTCCCACAGGCAG  
CGGCAAAAGCACCAAGGTCCCGGTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACT  
CAACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGAT  
CGATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTC-4200  
CACCTACGGCAAGTTCCTTGCCGACGGCGGGTGTCTGGGGGGCGCTTATGACATAATAAT  
TTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCGGCACTGTCCTTGA  
CCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTC  
CGTCACTGTGCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCC  
TTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGGAGACATCTCATCTTCTG-4500  
TCATTCAAAGAAGAAGTGGCAGCAACTCGCCGCAAGCTGGTCGCATTGGGCATCAATGC  
CGTGGGCTACTACCGCGGTCTTGACGTGTCCGTCACTCCGACCGAGCGGCGATGTTGTGCT  
CGTGGCAACCGATGCCCTCATGACCGGTATACCGGCGACTTCGACTCGGTGATAGACTG  
CAATACGTGTGTACCCAGACAGTCGATTTGAGCCTTGACCTACCTTCACCATTGAGAC  
AATCAGCTCCCCAGGATGCTGTCTCCGCACTCAACGTGCGGGCAGGACTGGCAGGGG-4800  
GAAGCCAGGCATCTACAGATTTGTGGCACCAGGGGAGCGCCCTCCGGCATGTTGCACTC  
GTCCGTCTCTGTGAGTGCTATGACGAGGCTGTGCTTGGTATGAGCTCAGCCCCGCCGA  
GACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCA  
CTTTGAATTTTGGGAGGGCGTCTTTACAGGCTCACTCATATAGATGCCCACTTTCTATC  
CCAGACAAAGCAGAGTGGGGAGAACCTTCTTACCTGGTAGCGTACCAAGCCACCGTGTG-5100  
CGTAGGGCTCAAGCCCTCCCCATCGTGGGACAGATGTGGAAGTGTGATTGCGCT  
CAAGCCCAACCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTGAGATGA  
AATCACCCTGACGCACCCAGTCACCAATACATCATGACATGCATGTCGGCCGACCTGGA  
GGTCGTACGAGCACCTGGGTGCTCGTTGGCGGCGTCTGGCTGCTTTGGCCGCGTATTG  
CCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCTGCTTGTCCGGGAAGCCGGCAAT-5400  
CATACCTGACAGGGAAGTCTCTACCGAGAGTTTCGATGAGATGGAAGAGTGCTCTCAGCA  
CTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGG  
CCTCTGCAGACCGCTCCCGTCAGGCAGAGGTTATCGCCCTGCTGTCCAGACCAACTG  
GCAAAAACCTCGAGACCTTCTGGGCGAAGCATATGTGGAACCTTCATCAGTGGGATACAATA  
CTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTAC-5700  
AGCTGCTGTACCAAGCCCACTAACCACTAGCCAAACCTCCTCTTCAACATATTGGGGGG  
GTGGGTGGCTGCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTT  
AGCTGGCGCCGCCATCGGCAGTGTGGACTGGGGAAGGTCTCATAGACATCTTGCAGG  
GTATGGCGCGGGCTGGCGGGAGCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCT  
CTCCACGGAGGACCTGGTCAATCTACTGCCCCGCACTCTCTCGCCGGAGCCCTCGTAGT-6000  
CGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCA  
GTGGATGAACCGGCTGATAGCCTTCGCTCCCGGGGGAACCATGTTTCCCCACGCACTA  
CGTGCCGGAGAGCGATGCAGCTGCCCCGCTCACTGCCATACTCAGCAGCCTCACTGTAAC  
CCAGCTCCTGAGGCGACTGCACCAAGTGGATAAGCTCGGAGTGTACCACTCATGCTCCGG  
TTCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTG-6300



FIG. 62C

GCTAAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCTGCCAGCGCGG  
GTATAAGGGGGTCTGGCGAGTGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGA  
GATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCTAGGACCTGCAGGAA  
CATGTGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCTGTACCCCCCTTCC  
TGC6CCGAACCTACACGTTCCGCTATGGAGGGTGTCTGCAGAGGAATATGTGGAGATAAG-6600  
GCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTCAAATGCCCGTG  
CCAGGTCCCATCGCCGAATTTTTACAGAATTGGACGGGGTGCCTACATAGGTTTGC  
GCCCCCTGCAAGCCCTTGTGCGGGAGGAGGTATCATTAGAGTAGGACTCCACGAATA  
CCCGGTAGGGTGCATTAACCTTGCAGGCCGAACCGGACGTGGCCGTGTTGACGTCCAT  
GCTCACTGATCCCTCCCATATAACAGCAGAGGGCGGGCGGAAGGTTGGCGAGGGGATC-6900  
ACCCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAAC  
TTGCACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAG  
GCAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAAAGTGGTGATTCTGGA  
CTCCTTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAAT  
CCTGCGGAAGTCTCGGAGATTTCGCCAGGCCCTGCCGTTTGGGCGCGGCCGACTATAA-7200  
CCCCCGCTAGTGGAGACGTGGAAAAAGCCGACTACGAACCACTGTGGTCCATGGCTG  
TCCGCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCTCGGAAGAAGCGGACGGTGGT  
CCTCACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTGCCACCAGAAGCTTTGGCAG  
CTCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCTTC  
TGCTGCCCCCCCGACTCCGACGCTGAGTCTATTCTCCATGCCCCCTGGAGGGGGA-7500  
GCCTGGGGATCCGGATCTTAGCGACGGGTATGGTCAACGGTCAGTAGTGAGGCCAACGC  
GGAGGATGTCTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTG  
CGCCGCGGAAGAACAGAACTGCCATCAATGCACTAAGCAACTCGTTGCTACGTACCA  
CAATTTGGTGTATTCCACCACCTACGCAAGTGTGCCAAAGGCAGAAAGTCACTT  
TGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGC-7800  
GGCGTCAAAAGTGAAGGCTAAGTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCC  
ACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAA  
GGCCGTAAACCCACATCAACTCCGTGTGGAAGACCTTCTGGAAGACAATGTAAACCAAT  
AGACACTACCATCATGGCTAAGAACGAGGTTTCTGCGTTTCAAGCTGAGAAAGGGGGTGC  
TAAGCCAGCTCGTCTCATCGTGTTCGCCGATCTGGGCGTGCAGGTGTGCGAAAAGATGGC-8100  
TTTGTACGACGTGGTTACAAAGTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCA  
ATACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCC  
AATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCG  
TACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCTGGCCATCAA  
GTCCCTCACCAGAGAGGCTTTATGTTGGGGGCCCTTTACCAATTCAAGGGGGGAGAACTG-8400  
CGGCTATCGCAGGTGCCGCGGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCAC  
TTGCTACATCAAGGCCCGGGCAGCTGTGAGCCGCGAGGGCTCCAGGACTGCACCATGCT  
CGTGTGTGGCGACGACTTAGTCTGTATCTGTGAAAGCGGGGGTCCAGGAGGACGCGGC  
GAGCCTGAGAGCCTTACGGAGGCTATGACCAGGTAATCCGCCCCCTGGGGACCCCC  
ACAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCAACGTGTAGTCGCCCA-8700  
CGACGGCGCTGGAAAGAGGGTCTACTACCTCACCCTGACCCTACAACCCCCCTCGCGAG  
AGCTGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCAT  
GTTTGGCCCCACACTGTGGGCGAGGATGATACTGATGACCATTTCTTAGCGTCTTAT  
AGCCAGGGACAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCTGCTACTCCAT  
AGAACCCTTGTATCTACCTCAATCATTCAAAGACTCCATGGCTCAGCGCATTTTCACT-9000  
CCACAGTTACTCTCAGGTGAAATTAATAGGGTGGCCGATGCCTCAGAAAACCTTGGGGT  
ACCGCCCTTGCAGGCTTGGAGACACCGGGCCGAGCGTCCGCGCTAGGCTTCTGGCCAG  
AGGAGGCAAGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAGCT  
CAAAC



FIG. 62D

1 CACTCCACCATGAATCACTCCCCTGTGAGGAACTACTGTCTTCACGCAGAAAGCGTCTAG  
GTGAGGTGGTACTTAGTGAGGGGACACTCCTTGATGACAGAAAGTGCCTCTTTCGCAGATC

61 CCATGGCGTTAGTATGAGTGTCTGTCAGCCTCCAGGACCCCCCTCCGGGGAGAGCCATA  
GGTACCGCAATCATACTCACAGCACGTGCGAGGTCTGGGGGGGAGGGCCCTCTCGGTAT

121 GTGGTCTGCGGAACCGGTGAGTACCCGGAATTGCCAGGACGACCGGGTCTTTTCTTGGA  
CACCAGACGCCCTTGGCCACTCATGTGGCCTTAACGGTCTGCTGGCCAGGAAAGAACCT

181 TCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCGCAAGACTGCTAGCCGAGTAGT  
AGTTGGGCGAGTTACGGACCTCTAAACCCGCACGGGGCGTTCTGACGATCGGCTCATCA

241 GTTGGGTGCGGAAAGGCCCTTGTGGTACTGCCTGATAGGGTGTGCGAGTGCCCCGGGAG  
CAACCCAGCGCTTTCGGGAACACCATGACGGACTATCCACGAACGCTCACGGGGCCCTC

301 GTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACCTCAAAAAAAAAACAAACGTAA  
CAGAGCATCTGGCAGTGGTACTCGTGCTTAGGATTTGGAGTTTTTTTTTTGTTTGCATT

361 CACCAACCGTCGCCCCACAGGACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGT  
GTGGTTGGCAGCGGGTGTCTGCAAGTTCAAGGGCCACCGCAAGTCTAGCAACCACCTCA

421 TTAATTGTTGCCGCGCAGGGGCCCTAGATTGGGTGTGCGCGCGACGAGAAAGACTTCCGA  
AATGAACAACGGCGCGTCCCCGGGATCTAACCACACGCGCGTGTCTTTCTGAAGGCT

481 GCGGTGCAACCTCGAGGTAGACGTGAGCCTATCCCAAGGCTCGTGGCCCCGAGGGCAG  
CGCCAGCGTTGGAGCTCCATCTGCAGTGCGATAGGGGTTCCGAGCAGCCGGGCTCCCGTC

541 GACCTGGGCTCAGCCCCGGGTACCCCTTGGCCCTCTATGGCAATGAGGGCTGCGGGTGGGC  
CTGGACCCGAGTCGGGGCCATGGGAACGGGGAGATAACGTTACTCCCGACGCCACCCG

601 GGGATGGCTCCTGTCTCCCCGTGGCTCTCGGCCCTAGCTGGGGCCCCACAGACCCCGGCG  
CCCTACCGAGGACAGAGGGGCACCGAGAGCCGGATCGACCCCGGGGTGTCTGGGGGCCG

661 TAGGTGCGCAATTTGGGTAAAGGTGATCGATACCCCTTACGTGCGGCTTCGCCGACCTCAT  
ATCCAGCGCGTTAAACCCATTCCAGTAGCTATGGGAATGCACGCCGAAGCGGCTGGAGTA

721 GGGGTACATACCGCTCGTGGCGCCCCCTTGGAGGCGCTGCCAGGGCCCTGGCGCATGG  
CCCCATGTATGGCGAGCAGCCGCGGGGAGAACTCCGCGACGGTCCCGGGACCGCTACC

781 CGTCCGGGTTCTGGAAGACGGCGTGAACCTATGCAACAGGGAACCTTCTGGTTGCTCTTT  
GCAGGCCCAAGACCTTCTGCCGCACTTGATACGTTGTCCCTTGGAAAGGACCAACGAGAAA

841 CTCTATCTTCTTCTGGCCCTGCTCTCTTGTGCTTACTGTGCCGCTTCGGCCTACCAAGT  
GAGATAGAAGGAAGACCGGACGAGAGAACGAACTGACACGGGCGAAGCGGATGGTTCA

901 GCGCAACTCCACGGGGCTTTACCACGTACCAATGATTGCCCTAACTCGAGTATTGTGTA  
CGCGTTGAGGTGCCCCGAAATGGTGCAGTGGTTACTAACGGGATTGAGCTCATAACACAT

961 CGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGCCTCCCTTGCCTTCTGAGGGCAA  
GCTCCGCCGGCTACGGTAGGACGTGTGAGGCCCCACGCAAGGGAACGCAAGCACTCCCGTT

1021 CGCCTCGAGGTGTTGGGTGGCGATGACCCCTACGGTGGCCACCAAGGATGGCAAACCTCC  
GCGGAGCTCCACAACCCACCGCTACTGGGGATGCCACCGGTGGTCCCTACCGTTTGAGGG

1081 CGCGACGCAAGCTTGCAGCTCACATCGATCTGCTTGTGCGGAGCGCCACCCTCTGTTCCGC  
GCGCTGCGTCGAAGCTGCACTGATGCTAGACGAACAACCCCTCGCGGTGGGAGACAAGCCG

1141 CCTCTACGTGGGGGACCTATGCGGGTCTGTCTTTCTTGTGCGGCAACTGTTACCTTCTC  
GGAGATGCACCCCTGGATACGCCAGACAGAAAGAACAGCCGTTGACAAGTGAAGAG

1201 TCCAGGCGCCACTGGACGACGCAAGGTTGCAATTGCTCTATCTATCCCGGCCATATAAC  
AGGGTCCGCGGTGACCTGCTGCGTTCAACGTTAACGAGATAGATAGGGCCGGTATATTG

1261 GGGTCACCGCATGGCATGGGATATGATGATGAAGTGGTCCCTACGACGGCGTTGGTAAT  
CCCAGTGGCGTACCGTACCCTATACTACTACTTGACCAGGGGATGCTGCCGCAACCATTA



FIG. 62E

1321 GGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGTCTACTGGGG  
CCGAGTCGACGAGGCCCTAGGGTGTTCGGTAGAACCTGTACTAGCGACCACGAGTGACCCC

1381 AGTCCTGGCGGGCATAGCGTATTTCTCCATGGTGGGGAACCTGGGCGAAGGTCTGCTAGT  
TCAGGACCGCCGTATCGCATAAAGAGGTACACCCCTTGACCCGCTTCAGGACCATCA

1441 GCTGCTGCTATTTGCCGGCGTCGACGCGGAAACCCACGTACCGGGGGAAGTGCCGGCCA  
CGACGACGATAAACGGCCGAGCTGCGCCTTTGGGTGCAGTGGCCCCCTTCACGGCCGGT

1501 CACTGTGTCTGGATTTGTTAGCCTCCTCGACCAGGCGCCAAGCAGAACGTCCAGCTGAT  
GTGACACAGACCTAAACAATCGGAGGAGCGTGGTCCGCGGTTCTGCTTGCAGGTGCGACTA

1561 CAACACCAACGGCAGTTGGCACCTCAATAGCACGGCCCTGAACTGCAATGATAGCCTCAA  
GTTGTGGTTGCCGTCAACCGTGGAGTTATCGTGCCGGGACTTGACGTTACTATCGGAGTT

1621 CACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGTTCAACTCTTCAGGCTGTCCTGA  
GTGGCCGACCAACCGTCCCAGAAAGATAGTGGTGTTCAGTTGAGAAGTCCGACAGGACT

1681 GAGGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACCAGGGCTGGGGCCCTATCAGTTA  
CTCCGATCGGTGACGCGCTGGGGAATGGCTAAACTGGTCCCGACCCCGGGATAGTCAAT

1741 TGCCAACGGAAGCGGGCCCCGACCAGCGCCCTACTGCTGGCACTACCCCCAAAACCTTG  
ACGGTTGCCTTCGCCGGGGCTGGTGCGGGGATGACGACCGTGATGGGGGGTTTTGGAAC

1801 CGGTATTGTCCCCGGAAGAGTGTGTGTGGTCCGGTATATTGCTTCACTCCAGCCCCGT  
GCCATAACACGGGCGCTTCTCACACACACAGGCCATATAACGAAGTGAGGGTCGGGGCA

1861 GGTGGTGGGAACGACCGACAGGTGCGGCGCGCCACCTACAGCTGGGGTGAAAATGATAC  
CCACCACCTTGCTGGCTGTCCAGCCGCGCGGGTGGATGTGACCCCACTTTTACTATG

1921 GGACGTCTTCGTCCTTAACAATACCAGGCCACCGCTGGGCAATTGGTTCCGTTGTACCTG  
CCTGCAGAAGCAGGAATTGTTATGGTCCGGTGGCGACCCGTTAACCAAGCCAACATGGAC

1981 GATGAACTCAACTGGATTACCAAAGTGTGCGGAGCGCCTCCTTGTCATCGGAGGGGC  
CTACTTGAGTTGACCTAAGTGGTTTCACACGCTCGCGGAGGAACACAGTAGCCTCCCCG

2041 GGGCAACAACACCCTGCACTGCCCCACTGATTGCTTCGCAAGCATCCGGACGCCACATA  
CCCGTTGTTGTGGGACGTGACGGGGTGACTAACGAAGGCGTTCTAGGCCTGCGGTGTAT

2101 CTCTCGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTGCCTGGTGGCTACCCGTATAG  
GAGAGCCACGCCGAGGCCAGGGACCTAGTGTGGGTCCACGGACAGCTGATGGGCATATC

2161 GCTTTGGCATTATCCTTGTAACATCACTACACCATATTTAAATCAGGATGTACGTGGG  
CGAAACCGTAATAGGAACATGGTAGTTGATGTGGTATAAATTTAGTCTACATGCACCC

2221 AGGGGTGGAACACAGGCTGGAAGCTGCCTGCAACTGGACGCGGGGCGAACGTTGCGATCT  
TCCCAGCTTGTGTCCGACCTTCGACGAGCTTGACCTGCGCCCCGCTTGCAACGCTAGA

2281 GGAAGACAGGGACAGGTCCGAGCTCAGCCGTTACTGCTGACCACTACACAGTGGCAGGT  
CCTTCTGTCCCTGTCCAGGCTCGAGTCGGGCAATGACGACTGGTGATGTGTACCGTCCA

2341 CCTCCCGTGTTCCTTCACAACCTACCAGCCTTGTCACCGGCCCTCATCCACCTCCACCA  
GGAGGGCACAAGGAAGTGTGGGATGGTCGGAACAGGTGGCCGGAGTAGGTGGAGGTGGT

2401 GAACATTGTGGACGTGCAGTACTTGACGGGGTGGGGTCAAGCATCGCGTCTGGGCCAT  
CTTGTAACACCTGCACGTGATGAACATGCCCCACCCAGTTCTGAGCGCAGGACCCGGTA

2461 TAAGTGGGAGTACGTCGTTCTCCTGTTCTTCTGCTTGCAGACGCGCGCTGCTGCTCTG  
ATTACCCCTCATGCAGCAAGAGGACAAGGAAGACGAACGTCTGCGCGCGCAGACGAGGAC

2521 CTTGTGGATGATGCTACTCATATCCAAGCGGAGGCGGCTTTGGAGAACCTCGTAATACT  
GAACACCTACTACGATGAGTATAGGGTTCGCTCCGCCGAAACCTCTTGAGCATTATGA

2581 TAATGCAGCATCCCTGGCCGGGACGACGGTCTTGATCCTTCTCGTGTCTTCTGCTT  
ATTACGTCGTAGGGACCGGCCCTGCGTGCCAGAACATAGGAAGGAGCACAAGAAGACGAA



FIG. 62F

2641 TGCATGGTATTTGAAGGGTAAGTGGGTGCCCCGAGCGGTCTACACCTTCTACGGGATGTG  
ACGTACCATAAACTTCCCATTCACCCACGGGCTCGCCAGATGTGGAAGATGCCCTACAC

2701 GCCTCTCCTCCTGCTCCTGTTGGCGTTGCCCCAGCGGGCGTACGCGCTGGACACGGAGGT  
CGGAGAGGAGGACGAGGACAACCGCAACGGGGTGGCCGATGCGCGACCTGTGCCTCCA

2761 GGCCGCGTCGTGTGGCGGTGTTGTTCTCGTCGGGTTGATGGCGCTGACTCTGTCAACATA  
CCGGCGCAGCACACCGCCACAACAAGAGCAGCCCACTACCGCGACTGAGACAGTGGTAT

2821 TTACAAGCGCTATATCAGCTGGTGTGTTGGTGGCTTCAGTATTTTCTGACCAGAGTGGGA  
AATGTTCCGATATAGTCGACCACGAACACCACCGAAGTCATAAAAGACTGGTCTACCT

2881 AGCGCAACTGCACGTGTGGATTCCCCCTCAACGTCCGAGGGGGGCGCGACGCCGTCTAT  
TCGCGTTGACGTGCACACCTAAGGGGGGAGTTGCAGGCTCCCCCGCGCTGCGGCAGTA

2941 CTTACTCATGTGTGCTGTACACCCGACTCTGGTATTTGACATACCAAATTGCTGCTGGC  
GAATGAGTACACACGACATGTGGGCTGAGACCATAAACTGTAGTGGTTTAAACGACGACC

3001 CGTCTTCGGACCCCTTTGGATTCTTCAAGCCAGTTTGCTTAAAGTACCCTACTTTGTGCG  
GCAGAAGCCTGGGGAAACCTAAGAAGTTCGGTCAAACGAATTTTCATGGGATGAAACACGG

3061 CGTCCAAGGCCCTTCTCCGGTTCTGCGGTTAGCGCGGAAGATGATCGGAGGCCATTACGT  
GCAGGTTCCGGAAGAGGCCAAGACGCGCAATCGCGCTTCTACTAGCTCCGGTAATGCA

3121 GCAAATGGTCATCATTAAAGTTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCAC  
CGTTTACCAGTAGTAATTCAATCCCGCGAATGACCGTGGATACAAATATTGGTAGAGTG

3181 TCCTCTTCGGGACTGGGCGCACAACGGCTTGCGAGATCTGGCCGTGGCTGTAGAGCCAGT  
AGGAGAAGCCCTGACCCGCGTGTGGCGAACGCTCTAGACCGGCACCGACATCTCGGTCA

3241 CGTCTTCTCCAAATGGAGACCAAGCTCATCACGTGGGGGGCAGATACCGCCGCGTGGCG  
GCAGAAGAGGGTTTACCTCTGGTTCGAGTAGTGACCCCCCGTCTATGGCGGCGCACGCC

3301 TGACATCATCAACGGCTTGCCTGTTTCCGCCGCGAGGGGCGGGAGATACTGCTCGGGCC  
ACTGTAGTAGTTGCCGAACGGACAAAGCGGGCGTCCCGGCCCTCTATGACGAGCCCGG

3361 AGCCGATGGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCCATCACGGCGTACGCCCA  
TCGGCTACCTTACCAGAGGTTCCCACTCCAACGACCGGGGTAGTGCCGCATGCGGGT

3421 GCAGACAAGGGGCTCCTAGGGTGCATAATCACCAGCCTAACTGGCCGGGACAAAAACCA  
CGTCTGTTCCCGGAGGATCCACGATTAGTGGTGGGATTGACCGGCCCTGTTTTTGGT

3481 AGTGGAGGGTGAGGTCCAGATTGTGTCAACTGCTGCCAAACCTTCTGGCAACGTGCAT  
TCACCTCCCACTCAAGGTCTAACACAGTTGACGACGGGTTTGAAGGACCGTTGCACGTA

3541 CAATGGGGTGTGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCATCGCGTACCCAA  
GTTACCCACACGACCTGACAGATGGTGCCCCGGCCTTGCTCCTGGTAGCGCAGTGGGTT

3601 GGGTCCTGTCATCCAGATGTATACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCC  
CCAGGACAGTAGGTCTACATATGGTTACATCTGGTTCTGGAACACCCGACCGGGCGAGG

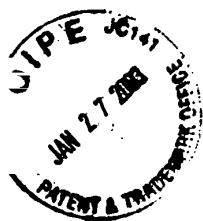
3661 GCAAGGTAGCCGCTCATTGACACCCTGCACTTGCGGCTCCTCGGACCTTTACCTGGTCAC  
GCTTCCATCGGGGAGTAACTGTGGGACGTGAACGCCGAGGAGCTGGAATGGACAGTG

3721 GAGGCACGCCGATGTCATTCCCGTGCGCCGGCGGGGTGATAGCAGGGGCGAGCTGTGTC  
CTCCGTGCGGCTACAGTAAGGGCACGCGGCCGCCCACTATCGTCCCGTGGACGACAG

3781 GCCCCGGCCCATTTCTACTTGAAAGGCTCCTCGGGGGTCCGCTGTTGTGCCCCGCGGG  
CGGGGCGGGTAAAGGATGAACCTTCCGAGGAGCCCCCAGGCGACAACAGGGGCGCCC

3841 GCACGCCGTGGGCATATTTAGGGCCGCGGTGTGCACCCGTGGAGTGGCTAAGGCGGTGGA  
CGTGCGGCACCCGTATAAATCCCGGCCACACGTGGGCACCTCACCGATTCCGCCACCT

3901 CTTTATCCCTGTGGAGAACCTAGAGACAACCATGAGGTCCCCGGTGTTCACGGATAACTC  
GAAATAGGGACACCTCTTGATCTCTGTTGGTACTCCAGGGGCCACAAGTGCCTATTGAG



## FIG. 62G

3961 CTCTCCACCAGTAGTGCCCCAGAGCTTCCAGGTGGCTCACCTCCATGCTCCACAGGCAG  
GAGAGGTGGTCATCACGGGGTCTCGAAGGTCCACCGAGTGGAGGTACGAGGGTGTCCGTG

4021 CGGCAAAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACT  
GCCGTTTTCTGTGGTTCCAGGGCCGACGTATACGTGAGTCCCGATATTCCACGATCATGA

4081 CAACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGAT  
GTTGGGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTA

4141 CGATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTA CT  
GCTAGGATTGTAGTCTGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAG

4201 CACCTACGGCAAGTTCTTGCCGACGGCGGGTCTCGGGGGGCGCTTATGACATAATAAT  
GTGGATGCCGTTCAAGGAACGGCTGCCGCCACGAGCCCCCGGAATACTGTATTATTA

4261 TTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCGGCACTGTCTTGA  
AACACTGCTCACGGTGAGGTGCTACGGTGTAGGTAGAACCGGTAGCCGTGACAGGAAC

4321 CCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTC  
GGTTCGTCTCTGACGCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAG

4381 CGTCACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCC  
GCAGTGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGG

4441 TTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTG  
AAAAATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCTCTGTAGAGTAGAAGAC

4501 TCATTCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTGCATTGGGCATCAATGC  
AGTAAGTTTCTTCTTACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACG

4561 CGTGGCCTACTACCGCGGTCTTGACGTGTCCGTATCCCGACCAGCGGCGATGTTGTCTG  
GCACCGGATGATGGCGCCAGAAGTGCACAGGCAGTAGGGCTGGTGCAGCGCTACAACAGCA

4621 CGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTG  
GCACCGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGAC

4681 CAATACGTGTGTACCCAGACAGTCGATTTACGCCTTGACCCTACCTTACCATTGAGAC  
GTTATGCACACAGTGGGTCTGTACGCTAAAGTCGGAAGTGGGATGGAAAGTGGTAACCTG

4741 AATCACGCTCCCCAGGATGCTGTCTCCGCACTCAACGTGCGGGCAGGACTGGCAGGGG  
TTAGTGCGAGGGGGTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCTGACCGTCCCC

4801 GAAGCCAGGCATCTACAGATTTGTGGCACCAGGGGGAGCGCCCTCCGGCATGTTGCACTC  
CTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGAGGGCGTACAAGCTGAG

4861 GTCCGTCCTCTGTGAGTGCTATGACGCAAGGCTGTGCTTGGTATGAGCTCAGCCCCGCGA  
CAGGCAGGAGACACTCAGGATACTGCGTCCGACACGAACCATACTCGAGTGCGGGCGGCT

4921 GACTACAGTTAAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCA  
CTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACAGGTCTTGCT

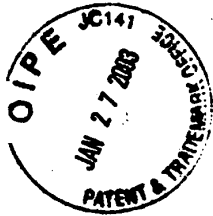
4981 TCTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATC  
AGAACTTAAACCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAG

5041 CCAGACAAAGCAGAGTGGGGAGAACCTTCTTACCTGGTAGCGTACCAAGCCACCGTGTG  
GGTCTGTTTCTGTCTCACCCCTCTTGGAAAGGAATGGACCATCGCATGGTTCGGTGGCACAC

5101 CGCTA66GCTCAAGCCCCCTCCCCATCGTGGGACCAGATGTGGAAGTGTGTTGATTGCGCT  
GCATCCCCGAGTTCGGGGAGGGGGTAGCACCTGGTCTACACCTTCAAACTAAGCGGA

5161 CAAGCCACCCCTCCATGGGCCAACCCCTGCTATACAGACTGGGCGCTGTTGAGAATGA  
GTTGCGGTGGGAGGTACCCGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACT

5221 AATCACCCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTGCGCCGACCTGGA  
TTAGTGGGACTGCGTGGGTGAGTGGTTTATGTAGTACTGTACGTACGCGGCTGGACCT



## FIG. 62H

5281 GGTGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTG  
CCAGCAGTGTCTGTTGGACCCACGAGCAACCGCCGAGGACCGACGAAACGGGCGCATAAC

5341 CCTGTCAACAGGCTGCGTGGTATAGTGGGACGGGTGCTCTTGTCCGGGAAGCCGGCAAT  
GGACAGTTGTCCGACGCACCAAGTATCACCCGTCCAGCAGAACAGGCCCTTCGGCCGTTA

5401 CATACTGACAGGGAAGTCTCTACCGAGAGTTGATGAGATGGAAGAGTGCTCTCAGCA  
GTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCAGGAGTCTGT

5461 CTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGG  
GAATGGCATGTAGCTCGTTCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCGGGAGCC

5521 CCTCTGACAGCCGCTCCCGTCAGGCAGAGTTATCGCCCTGCTGTCCAGACCAACTG  
GGAGGACGTCTGGCGCAGGGCAGTCCGTCTCAATAGCGGGACGACAGGTCTGGTTGAC

5581 GCAAAAACCTCGAGACCTTCTGGGCGAAGCATATGTGGAACCTTCATCAGTGGGATACAATA  
CGTTTTTGAAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTACCCTATGTTAT

5641 CTTGGCGGGCTTGTCAACGCTGCTGGTAACCCGCCATTGCTTCATTGATGGCTTTTAC  
GAACCGCCCGAACAGTTGCGACGGACATTGGGGCGGTAACGAAGTAACCTACCGAAAATG

5701 AGCTGCTGTACACAGCCCACTAACCCTAGCCAAACCTCCTCTTCAACATATTGGGGGG  
TCGACGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCC

5761 GTGGGTGGCTGCCAGCTCGCCGCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTT  
CACCCACCGACGGGTGAGCGGGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAA

5821 AGCTGGCGCCGCTATCGGCAGTGTGGACTGGGGAAGGTCCTCATAGACATCCTTGACGG  
TCGACCGCGGGGTAGCCGTCAACCTGACCCCTTCAGGAGTATCTGTAGGAACGTCC

5881 GTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCC  
CATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGG

5941 CTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGT  
GAGGTGCCTCCTGGACCAAGTTAGATGACGGGCGGTAGGAGAGCGGGCTCGGGAGCATCA

6001 CGGCGTGGTCTGTGACGAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCA  
GCCGACCAAGACAGTCGTTATGACGCGGGCGTGCAACCGGGCCCGCTCCCCGTACGT

6061 GTGGATGAACGGCTGATAGCCTTCGCTCCCGGGGAACCATGTTTCCCCACGCACTA  
CACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAAGGGGTGCGTGAT

6121 CGTGCCGGAGAGCGATGCAGCTGCCGCGCTCACTGCCATACTCAGCAGCCTCACTGTAAC  
GCACGGCCTCTCGCTACGTGACGGGCGCAGTGACGGTATGAGTCTCGGAGTGACATTG

6181 CCAGCTCCTGAGGCGACTGCACCAAGTGGATAAGCTCGGAGTGTAACCTCCATGCTCCGG  
GGTCGAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCC

6241 TTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTG  
AAGGACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACCTCGTGAAATTCTGGAC

6301 GCTAAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGG  
CGATTTTCGATTGAGTACGGTGTGACGGACCCCTAGGGGAAACACAGGACGGTTCGCGCC

6361 GTATAAGGGGGTCTGGCGAGTGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGA  
CATATTTCCCCAGACCGCTCACCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACT

6421 GATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCTAGGACCTGCAGGAA  
CTAGTGACCTGTACAGTTTTTGCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTT

6481 CATGTGGAGTGGGACCTTCCCATTAATGCCTACACCACGGGCCCCCTGTACCCCCCTTCC  
GTACACCTCACCTGGAAGGGGTAAATTACGGATGTGGTGCCCGGGACATGGGGGGAAGG

6541 TGCGCCGAACCTACAGTTTCGCGCTATGGAGGGTGTCTGCAGAGGAATATGTGGAGATAAG  
ACGCGGCTTGATGTGCAAGCGCGATACCTCCACAGACGTCTCCTTATACACCTCTATTCT





## FIG. 621

6601 GCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTCAAATGCCCGTG  
CGTCCACCCCTGAAGGTGATGCACTGCCATACTGATGACTGTTAGAGTTTACGGGCAC

6661 CCAGGTCCCATCGCCGAATTTTTACAGAATTGGACGGGGTGCCTACATAGGTTTGC  
GGTCCAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACG

6721 GCCCCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTGAGAGTAGGACTCCACGAATA  
CGGGGGGACGTTGCGGAACGACGCCCTCCTCCATAGTAAGTCTCATCTGAGGTGCTTAT

6781 CCCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCAGGACGTGGCCGTGTTGACGTCCAT  
GGGCCATCCCAGCGTTAATGGAACGCTCGGGCTTGGCTGCACCGGCACAACTGCAGGTA

6841 GCTCACTGATCCCTCCATATAACAGCAGAGGCGGGCGGCGAAGGTTGGCGAGGGGATC  
CGAGTGACTAGGGAGGGTATATTGTCGTCTCGCCGGCCCGCTTCCAACCGCTCCCTAG

6901 ACCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAAC  
TGGGGGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTG

6961 TTGCACCGCTAACCATGACTCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAG  
AACGTGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTC

7021 GCAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGA  
CGTCTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTCACCACTAAGACCT

7081 CTCCTTCGATCCGCTTGTTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCGAGAAAT  
GAGGAAGCTAGGCGAACACCGCCTCCTCTGCTCGCCCTTAGAGGCATGGGCGTCTTTA

7141 CCTGCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCGTTTGGGCGGGCCGACTATAA  
GGACGCCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAACCCGCGCGGCCGCTGATATT

7201 CCCCCGCTAGTGGAGACGTGGAAAAAGCCGACTACGAACCACCTGTGGTCCATGGCTG  
GGGGGGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAAGGTACCGAC

7261 TCCGCTTCCACCTCCAAAGTCCCCTCCTGTGCTCCTCGGCTCGGAAGAAGCGGACGGTGGT  
AGGCGAAGGTGGAGGTTTACGGGGAGGACACGGAGGCGGAGCCTTCTTCGCTGCCACCA

7321 CCTCACTGAATCAACCCTATCTACTGCCTTGCCCGAGCTCGCCACCAGAAGCTTTGGCAG  
GGAGTGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTC

7381 CTCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCCGCCCTTC  
GAGGAGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAAG

7441 TGGCTGCCCCCGACTCCGACGCTGAGTCCTATTCTCCATGCCCCCTGGAGGGGGGA  
ACCGACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCT

7501 GCCTGGGGATCCGGATCTTAGCGACGGGTGATGGTCAACGGTCAGTAGTGAGGCCAACGC  
CGGACCCCTAGGCCTAGAATCGCTGCCAGTACCAGTTGCCAGTCATCACTCCGTTGCG

7561 GGAGGATGTCGTGTGCTGCTCAATGTCTTACTCTTGACAGGCGCACTCGTCACCCCGTG  
CCTCTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCAC

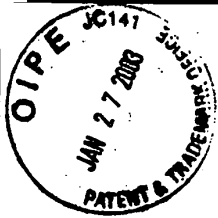
7621 CGCCGCGGAAGAACAGAACTGCCATCAATGCACTAAGCAACTCGTTGCTACGTACCA  
GCGGCGCCTTCTGTCTTTGACGGGTAGTTACGTGATTGTTGAGCAACGATGCAGTGGT

7681 CAATTTGGTGTATTCCACCACCTCACGCACTGCTTGCCAAAGGCAGAAAGAGTCACATT  
GTTAAACCACATAAGGTGGTGGAGTGCCTCACGAACGGTTTCCGTCTTCTTCAGTGTA

7741 TGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTAAGGAGGTTAAAGCAGC  
ACTGTCTGACGTTCAAGACCTGTGCGTAATGGTCTGATGAGTTCTCCAATTTCTGTCG

7801 GCGGTCAAAAGTGAAGGCTAAGTGTATCCGTAGAGGAAGCTTGACGCTGACGCCCC  
CCGACGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTGAACGTGCGACTGCGGGGG

7861 ACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAA  
TGTGAGTCGGTTTGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTT



## FIG. 62J

7921 GGCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAAT  
CCGGCATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTA

7981 AGACACTACCATCATGGCTAAGAAGAGGTTTTCTGCGTTAGCCTGAGAAGGGGGGTCG  
TCTGTGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCAGC

8041 TAAGCCAGCTCGTCTCATCGTGTCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGC  
ATTGCGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCG

8101 TTTGTACGACGTGGTTACAAAGCTCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCA  
AAACATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCTTCGAGGATGCCTAAGGT

8161 ATACTACCAAGGACAGCGGGTTGAATTCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCC  
TATGAGTGGTCTGTGCGCCAACCTAAGGAGCACGTTGCGACCTTCAGGTTCTTTTGGGG

8221 AATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCG  
TTACCCCAAGAGCATACTATGGGCGACGAACTGAGGTGTCACTGACTCTCGCTGTAGGC

8281 TACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCAAGCCCCGCGTGCCCATCAA  
ATGCCTCTCCGTTAGATGTTTACAACACTGGAGCTGGGGGTTGCGGCGACCGGTAGTT

8341 GTCCCTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTG  
CAGGGAGTGGCTCTCCGAAATACAACCCCGGGGAGAAAGTTAAGTTCCCCCTCTTGAC

8401 CGGCTATCGCAGGTGCCGCGGAGCGGCGTACTGACAAGTACTGTTGTTAAGTACACCTCAC  
GCCGATAGCGTCCACGGCGCGCTCGCCGATGACTGTTGATCGACACCATGTGGGAGTG

8461 TTGCTACATCAAGGCCCGGGCAGCCTGTGAGCCGCGAGGGCTCCAGGACTGCACCATGCT  
AACGATGTAGTTCCGGGCGCGTGGACAGCTCGGCGTCCCGAGGTCTGACGTGGTACGA

8521 CGTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGC  
GCACACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCAGGTCTCTGCGCCG

8581 GAGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTAATCCGCCCCCTGGGGACCCCCC  
CTCGGACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGACCCCTGGGGGG

8641 ACAACCAGAATACGACTTGGAGCTCATAACATCATGCTCTCCAACGTGTAGTCGCCCCA  
TGTTGGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGT

8701 CGACGGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAG  
GCTGCCGCGACCTTTCTCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGAGCGCTC

8761 AGCTGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCAT  
TCGACGCAACCTCTGTGCTTCTGTGTGAGGTGAGTTAAGGACCGATCCGTTGTATTAGTA

8821 GTTTGCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCTTAT  
CAAACGGGGGTGTGACACCCGCTCTACTATGACTACTGGGTAAAGAAATCGCAGGAATA

8881 AGCCAGGGACAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCTGCTACTCCAT  
TCGGTCCCTGGTGAACCTGTCCGGGAGCTAACGCTTAGATGCCCGGACGATGAGGTA

8941 AGAACCCTTGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACT  
TCTTGGTGAAGTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGA

9001 CCACAGTACTCTCCAGGTGAAATTAATAGGGTGGCCGATGCCTCAGAAAACCTTGGGGT  
GGTGTCAATGAGAGGTCCACTTTAATTATCCCACCGGCGTACGGAATCTTTGAACCCCA

9061 ACCGCCCTTGCGAGCTTGGAGACACCGGGCCCGAGCGTCCGCGCTAGGCTTCTGGCCAG  
TGGCGGGAACGCTCGAACCTCTGTGCCCCGGGCTCGCAGGCGGATCCGAAGACCGGTG

9121 AGGAGGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGAGTAAGAACAAAGCT  
TCCTCCGTCCCGACGGTATACACCGTTTATGGAGAAGTTGACCCGTCATTCTTGTTCGA

9181 CAAAC  
GTTTG

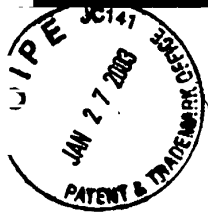
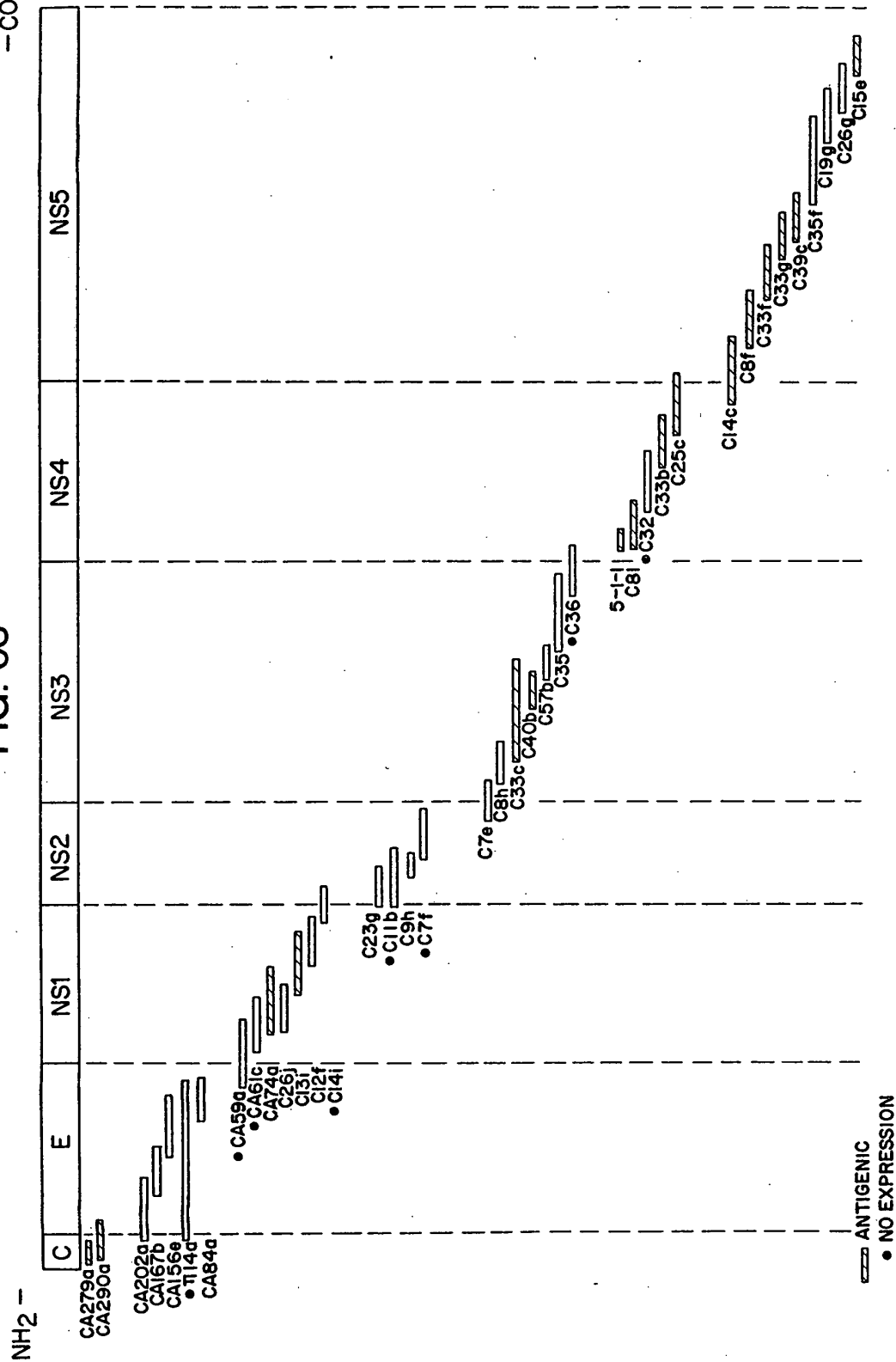


FIG. 63

-COOH



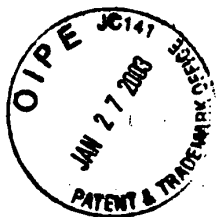
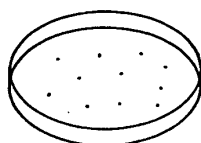


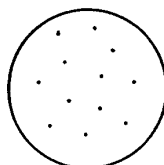
FIG. 64

TRANSFORM E coli WITH RECOMBINANT PLASMIDS

↓ (BLOT BACTERIA ON  
NITROCELLULOSE FILTER)



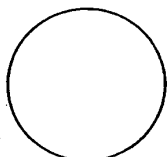
IPTG PLATE



LYSE WITH CHLOROFORM



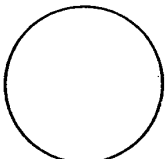
BSA ABSORPTION/DNAse/LYSOZYME



INCUBATE WITH PRIMARY  
ANTIBODY



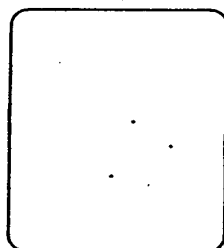
WASH



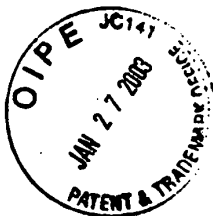
INCUBATE WITH  
 $^{125}\text{I}$  SECONDARY ANTIBODY



WASH



AUTORADIOGRAPH



	EXPRESSION LEVEL	CHIMPS			CHRONIC HCV PATIENT C100 POSITIVE								CHRONIC HCV PATIENT C100 NEGATIVE								CONVULSANT C100 NEGATIVE	COMMUNITY AC					
		1 POST ACUTE	2 POST ACUTE	3 C100 CONVERSION																		1 C100(+)	2 C100(+)	3 C100(-)	4 C100(-)	5 C100(-)	
					1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8							
SOD	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
CA259a	-	-	-	-	-	-	-	-	+	+	+	+	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-
CA290a	-	-	-	-	-	-	-	-	+	+	+	+	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-
CA202a	N.T.	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
CA167a	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
CA156C	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
π14a	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
CA84a	±	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
CA59a	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
CA61C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
CA74a	+	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C26j	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C13i	±	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C12f	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C14i	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C23g	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C11b	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C9h	±	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C7f	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C7e	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C8h	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C33c	+	+	±	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	±	+	+	+	±	-	
C40g	±	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C37b	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C35	±	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C36	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
5-11	+	-	-	+	±	+	+	+	+	+	+	+	-	-	-	-	+	+	+	+	+	+	±	+	+	-	
C8i	+	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	
C32	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C33b	-	-	-	-	-	-	-	+	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C25c	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	
C14c	+	-	-	±	-	-	-	-	-	-	-	-	+	-	+	-	-	-	-	-	+	+	+	-	-	-	
C8f	±	-	-	+	-	+	+	+	+	+	+	+	+	-	-	-	+	-	-	-	+	+	+	-	-	-	
C33f	-	-	-	-	-	+	+	-	-	-	+	+	-	-	-	-	-	-	+	-	+	+	-	-	-	-	
C33g	±	-	-	-	-	+	-	-	-	-	+	+	-	-	-	-	-	-	-	-	+	+	+	-	-	-	
C39c	+	-	-	-	-	+	-	-	-	-	+	-	-	-	-	-	-	-	-	-	+	+	+	-	-	-	
C35f	N.T.	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C19g	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C26g	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C15e	±	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	±	-	-	-	-	-	

N.T. = EXPRESSION NOT TESTED  
 ± THIS POLYPEPTIDE WAS NEGATIVE IN THIS COLONY SCREEN BUT POSITIVE BY WESTERN BLOT ANALYSIS

FIG. 65



## FIG. 66A

R T  
MSTNPKPQKKNRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATR  
KTSERSQPRGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSP-100  
RGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARA

T  
LAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGL-200  
YHVTNDCPNSSIVYEAADAILHTPGVPCVREGNASRCWVAMTPTVATRD  
GKLPATQLRRHIDLLVGSATLCSALYVGDLCSVFLVGQLFTFSPRRHWT-300

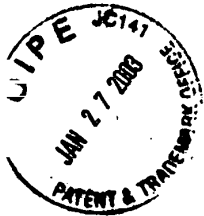
V  
TQGCNCSIYPGHITGHRMAWDMMMNWSPTTALVMAQLLRIPQAILDMIAG  
AHWGVLAGIAYFSMVGNWAKVLVLLLFAGVDAETHVTGGSAGHTVSGFV-400  
SLLAPGAKQNVQLINTNGSWHLNSTALNCNDSLNTGWLAGLFYHHKFNS  
GCPERLASCRPLTDFDQGWGPISYANGSGPDQRPYCWHPKPCGIVPAK-500  
SVCGPVYCFTSPVVGTTDRSGAPTYSWGENDTDFVFLNNTRPPLGNWF  
GCTWMNSTGFTKVCGAPPCVIGGAGNNTLHCPTDCFRKHPDATYSRCGSG-600

I  
PWLTPRCLVDYPYRLWHYPCTINYTIFKIRMYVGGVEHRLEAACNWTRGE  
RCDLEDRDRSELSPLLLTTTQWQVLPCSFTTLPALSTGLIHLHQNIYDVQ-700  
YLYGVGSSIASWAIKWEYVLLFLLADARVCSCWMLLI SQAEAALEN  
LVILNAASLAGTHGLVSFLVFFCFAWYLGKQWVP GAVYTFYGMWPLLLLL-800

(N)  
LALPQRAYALDTEVAASCGGVVLVGLMALTLSPYYKRYISWCLWWLQYFL  
TRVEAQLHVWIPPLNVRGGRDAVILLMCAVHPTLVFDITKLLLA VFGPLN-900  
ILQASLLKVYPFVRVQGLLRFCALARKMIGGHYVQMVIKLGALTGTYY  
NHLTPLRDWAHNGLRDLAVAVEFVVSQMETKLITWGADTAACGDIINGL-1000  
PVSARRGREILLGPADGMVSKGWRLLAPITAYAQQTRGLLGCIITSLTGR  
DKNQVEGEVQIVSTAAQTTFATCINGVCWTVYHGAGTRTIASPKGPVIQM-1100  
YTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRGDSRG  
SLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEN-1200  
LETTMRSPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAAGGYK

L  
VLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFL-1300  
ADGGCSCGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLATAT  
PPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGRHLIFCHSKKKC-1400  
DELA AKLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDS

Y (S)  
VIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSRTQRRGRTGRGKPGIYR-1500  
FVAPGERPSGMFDSVLC EYDAGCAWYELTPAETTVRLRAYMNTPLPV  
CQDHLEFWEGVFTGLTHIDAHFLSQTQSGENLPYL VAYQATVCARAQAP-1600  
PPSWDQMWKCLIRLKPTLHGPTLLYRLGAVQNEITLTHPVTKYIMTCS  
ADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRVLSGKPAIIPDREV-1700  
LYREFDEMEECQHLPIYIEQGMMLAEQFKQKALGLLQTASRQAEVIAPAV  
QTNWQKLETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAFTA AVTSP-1800  
LTTSQLLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLID



## FIG. 66B

(G)  
ILAGYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVCVAA-1900

(HC)  
ILRRHVGPGEAVQWMNRLIAFASRGNHVSPTHYVPESDAAARVAILSS  
LTVTQLLRRLHQWISSECTTPCSGSLRDIWDWICEVLSDFKTWLKAKLM-2000

(V)  
PQLPGIPFVSCQRGYKGVWRGDGIMHTRCHCGAEITGHVKNGTMRIVGPR  
TCRNMWSGTFPINAYTTGPCTPLPAPNYTFALWRVSAEEYVEIRQVGDH-2100  
YVTGMTTDNLKPCQVPSPEFFTEL DGVRLHRFAPPCKPLLREEVSFRVG  
LHEYPVGSQLPCEPEPDVAVLTSM LTPSHITAEAGRRRLARGSPPSVAS-2200  
SSASQLSAPSLKATCTANHDSPDAEL IEANLLWRQEMGGNITRVESENKV  
VILDSFDPLVAEEDEREISVPAEILRKSRRFAQALPVWARPDPYNPLVET-2300

S  
WKKPDYEPVHVGCPLPPPKSPPVPPPRKKRTVVLTESTLSTALAEATR

(FA)  
SFGSSSTSGITGDNTTTSSEPAPSGCPPDSDAESYSSMPPLEGEPGDPDL-2400  
SDGSWSTVSSEANAEDVVCCMSYSWTGALVTPCAAEEQKLPINALSNL  
LRHNLVYSTTSRSACQRQKKVTFDR LQVLDSHYQDVLKEVKAAASKVKA-2500

(F)  
NLLSVEEACSLTPPHSAKSKFGYGAKDVRCHARKAVTHINSVWKDLEDN  
VTPIDTTIMAKNEVFCVQPEKGGKPARLIVFPDLGVRVCEKMALYDVVT-2600  
KLPLAVMGSSYGFQYSPGQRVEFLVQAWKSKKTPMGFSYDTRCFDSTVTE

(G)  
SDIRTEEAIYQCCDLDPQARVAIKSLTERLYVGGPLTNSRGENCYRRCR-2700  
ASGVLTTSCGNTLTICYIKARAACRAAGLQDCTMLVCGDDLVCESAGVQ  
EDAASLRAFTEAMTRYSAAPPDPPQPEYDLELITSCSSNVSAHDGAGKR-2800  
VYYLTRDPTTPLARAAWETARHTFVNSWLGNIIMFAPTLWARMILMTHFF  
SVLIARDQLEQALDCEIYGACYSIEPLDLPPIIQRHLGLSAFSLHSYSPG-2900

G  
EINRVAACLRKLGVPPLRAWHRARSVRARLLARGGAAICGKYLFWAV  
RTKLK----- (Stop codon not yet reached)

( ) = Heterogeneity due to possible 5' or 3' terminal cloning artefacts.

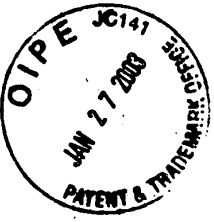


FIG. 67A

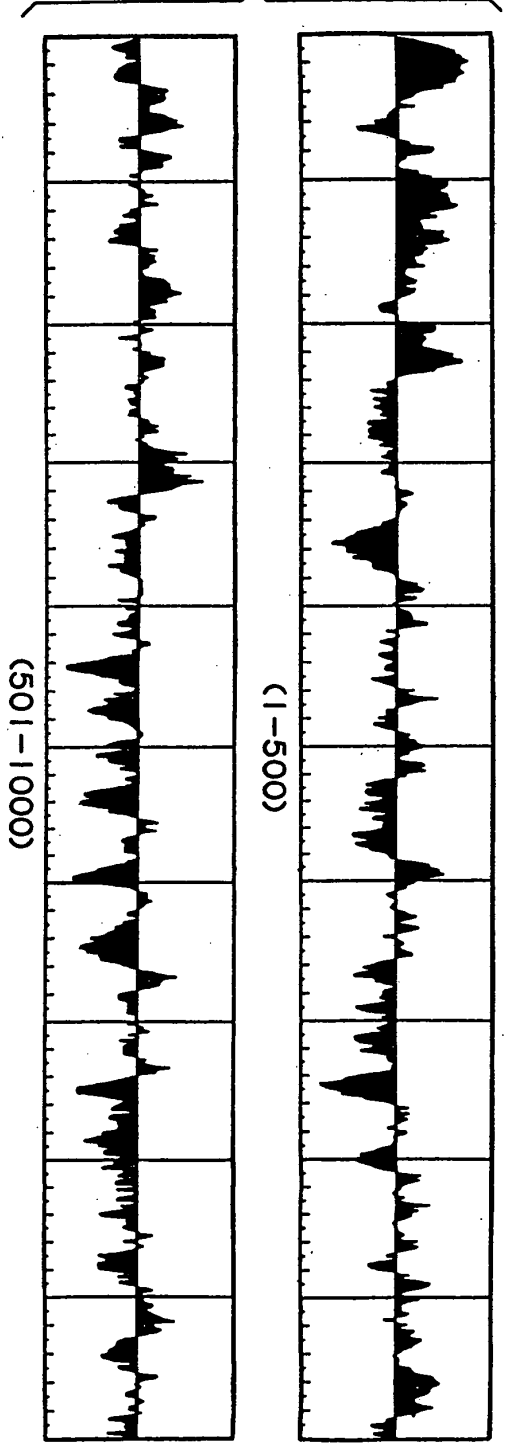
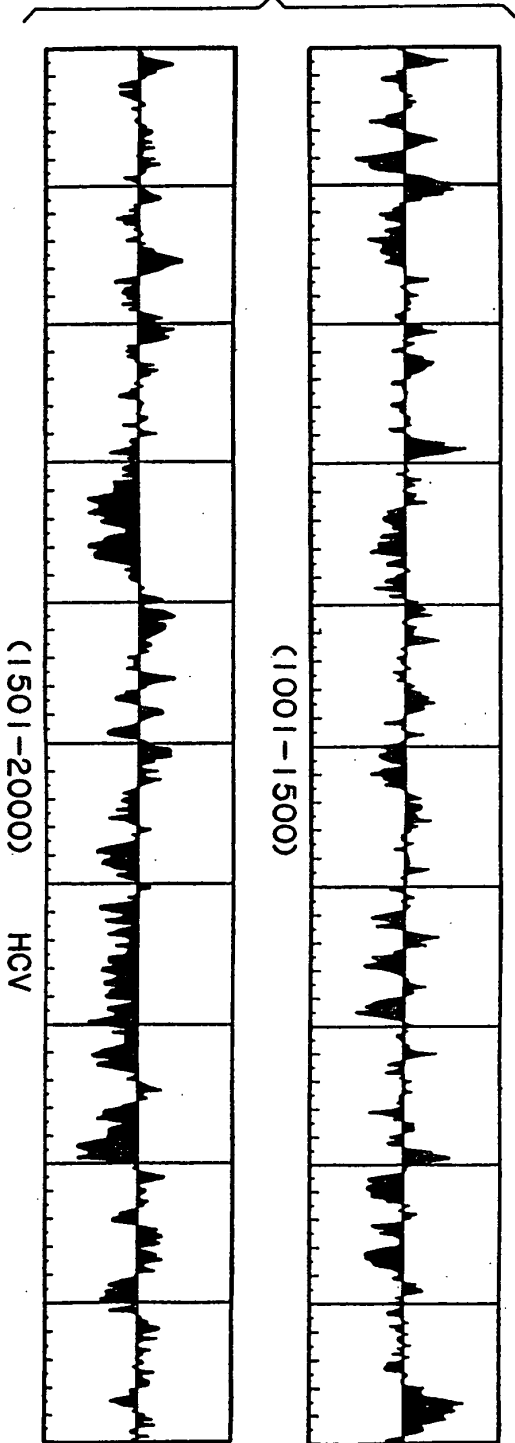


FIG. 67B



(1501-2000) HCV



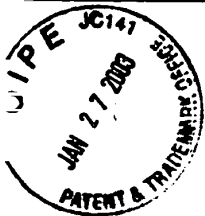


FIG. 67C

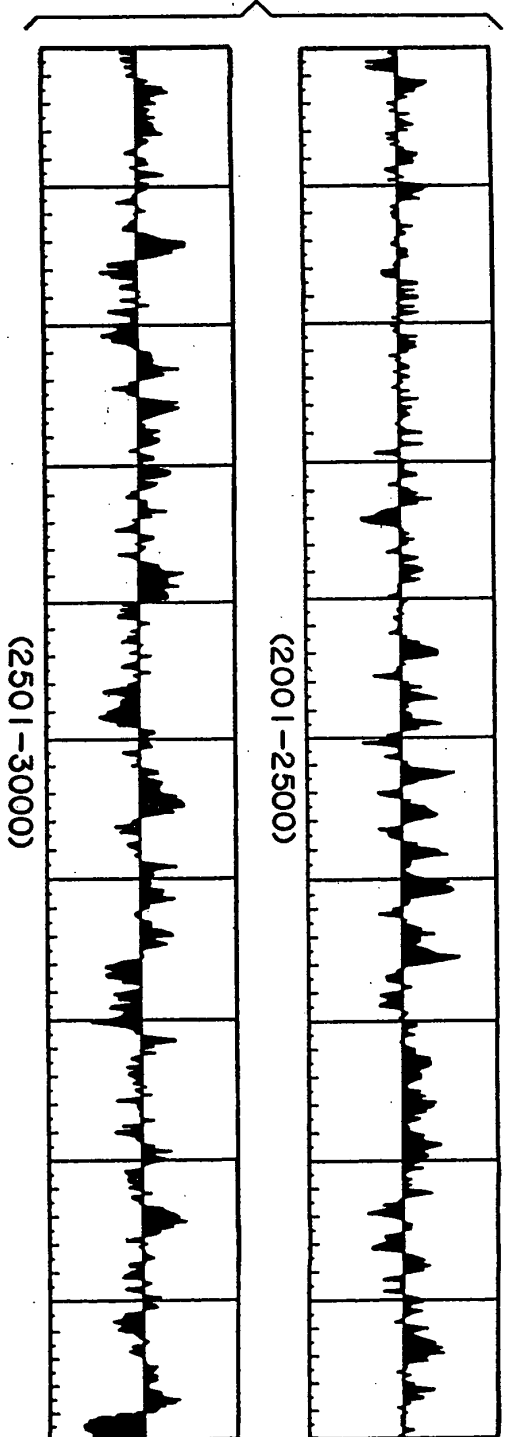
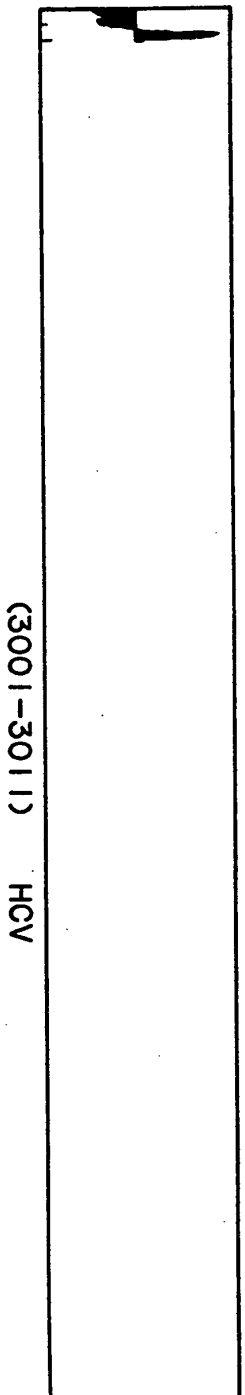


FIG. 67D



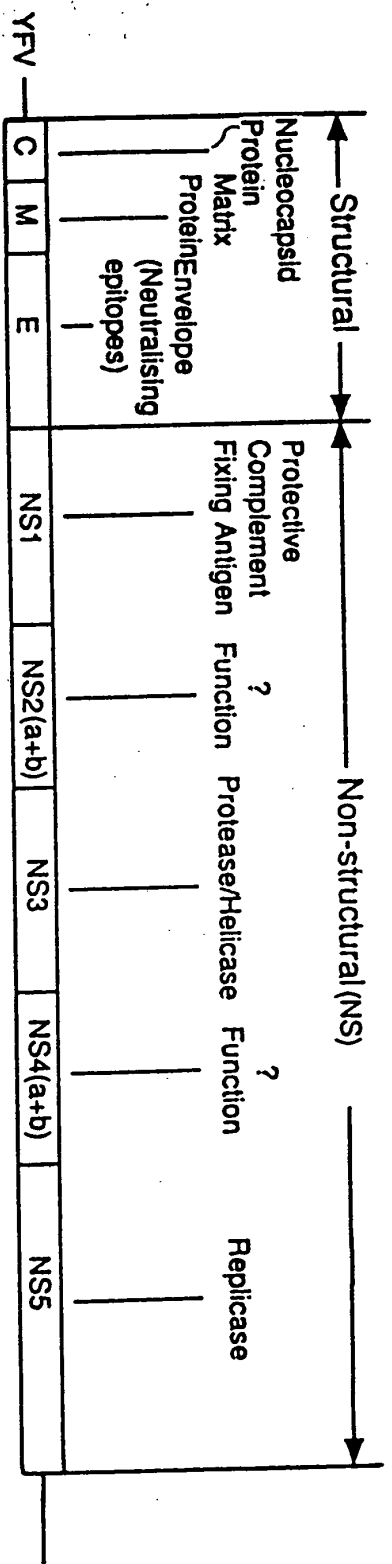


FIG. 69

☐ 5-1-1  
☐ C100



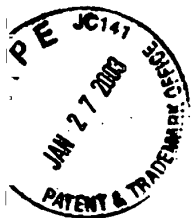


FIG. 68

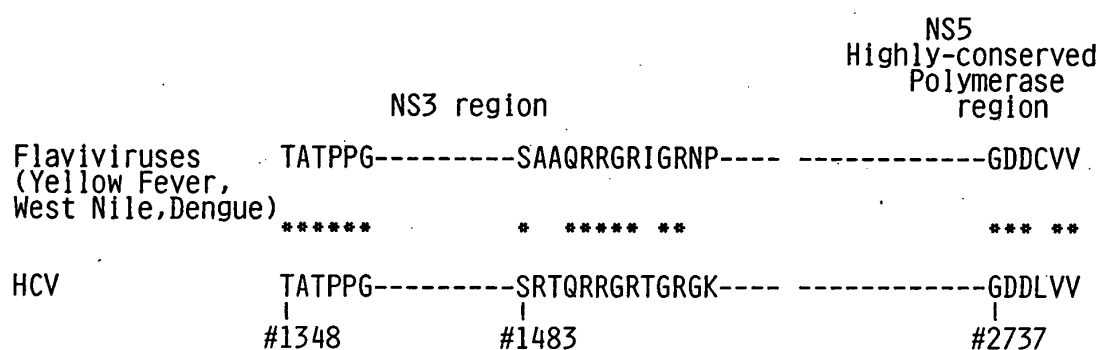


FIG. 73

5' CCGGGCGAGGGGGCAGTGCAGTGGATGAACGGCTGATAGCCTTCGCCTCCCGGGGGAAC 3'

3' CGCTCCCCGTCACGTCACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTG 5'

5' CATGTTTCCCCCTAATGAG 3'

3' GTACAAAGGGGGATTACTCAGC 5'

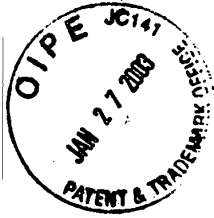


FIG. 70

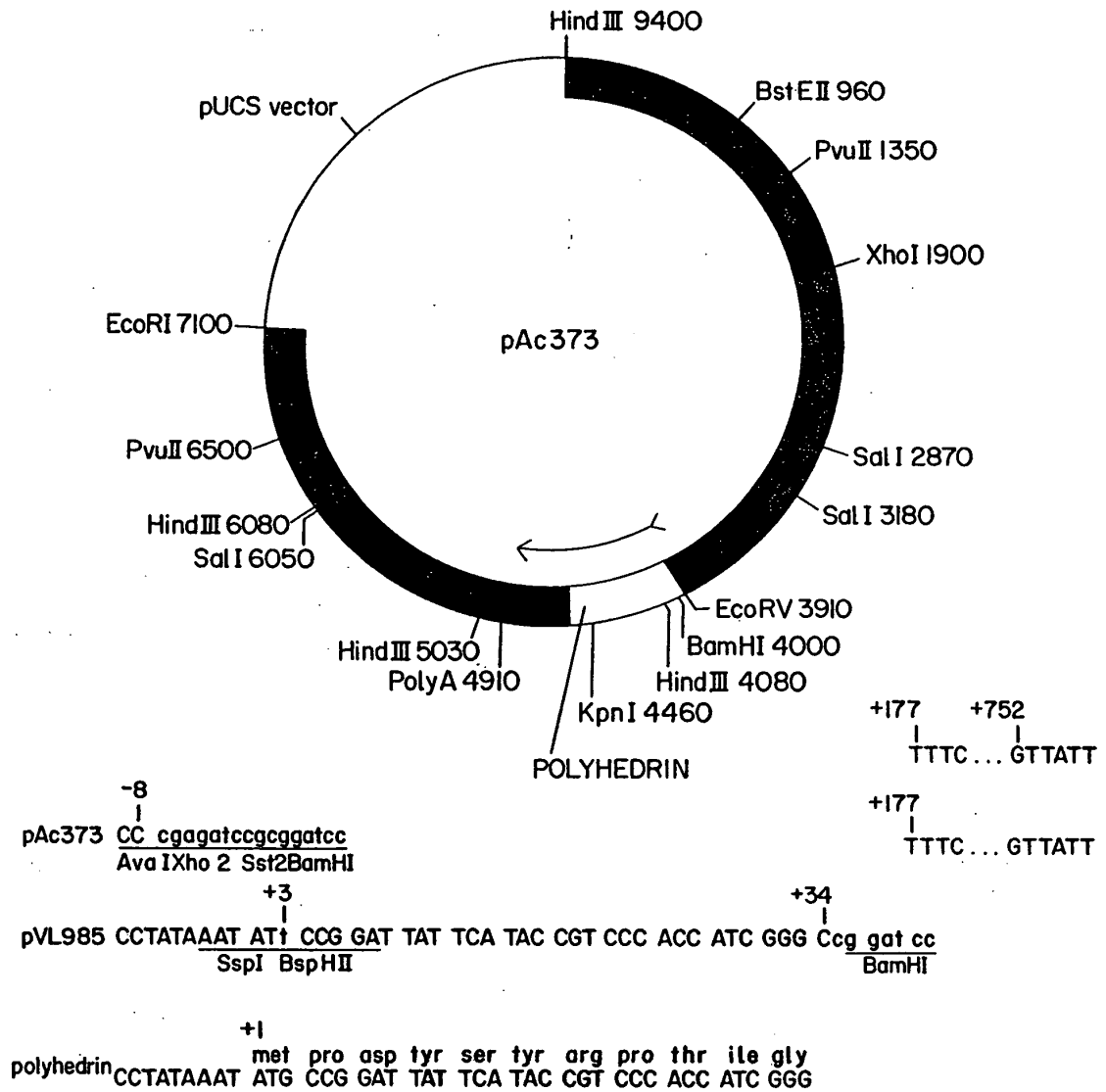
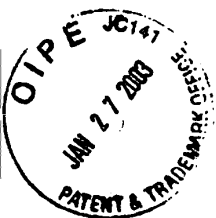


FIG. 71

-----Overlap with 16jh-----  
 GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys  
 GGCAGGGCTGCCATATGTGCCAAGTACCTCTTCAACTGGCAGTAAGAACAAAGCTCAA  
 CCGTCCCGACGGTATACACCGTTTCATGGAGAAGTTGACCCGTCATTCTTGTTCAGATT  
 -  
 LeuThrProIleAlaAlaIleGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr  
 CTCACTCCCAATAGCGCGCTGCCAGCTGGAAGTTGTCGGCTGTTACAGGCTGGCTAC  
 GAGTCAGGTTATCGCCGGCGACCGCTCGACCTGAACAGCGCCGACCAAGTCCCGACCGATG  
 61  
 SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys  
 AGCGGGGAGACATTATCACAAGCTGTCTCATGCCCGCCGCCGCTGATCTGTTTGC  
 121 TCGCCCCCTCTGTAATAAGTGTCCGACAGAGTACGGCCCGGGCCGACCTAGACCAAAACG  
 181 CC  
 CG

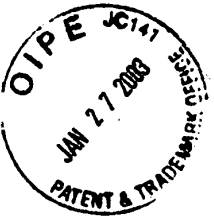
FIG. 72A

MetSerThrAsnProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGln  
 1 ATGAGCACGAATCCCTAAACCTCAAAAAAACAACGTAACACCAACCGTCGCCACAG  
 TACTCGTCTTAGGATTGGAGTTTTTTTTTTTGTGTCATTGTGTTGGCAGCGGGTGTCTC  
 AspValLysPheProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArg  
 61 GACGTCAAGTTCCTGGGTGGCGGTCAAGATCGTTGGTGAGTTTACTTGTGCGCGCAGG  
 CTGCAGTTCAAGGGCCACCGCCAGTCTAGCAACCACTCAAAATGAACACACGGCGGTCC



# FIG. 72B

121 GLYProArgLeuGlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGly  
 GGCCCTAGATTGGGTGTGCGCGCAGACGAGAAGACTTCGAGCGGTCCCAACCTCGAGGT  
 CCGGATCTAACCCACACGCGCGCTGCTCTTCTGAAGGCTCGCCAGCGTTGGAGCTCCA  
  
 181 ArgArgGlnProIleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGly  
 AGACGTCAGCCCTATCCCCAAGGCTCGTCGCGCCGAGGGCAGGACCTGGGCTCAGCCCGG  
 TCTGCAGTCGGATAGGGGTTCGAGCAGCCGGGCTCCCGTCTGGAACCCGAGTCGGGGCC  
  
 241 TyrProTrpProLeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerPro  
 TACCTTGGCCCTCTATGCAATGAGGCGTGGGGTGCGGATGGCTCCTGCTCC  
 ATGGGAACCGGGAGATACCGTTACTCCCGACGCCACCCGCTTACCGAGGACAGAGGG  
  
 301 ArgGlySerArgProSerTrpGlyProThrAspProArgArgSerArgAsnLeuGly  
 CGTGGCTCTCGGCTAGCTGGGGCCCCACAGACCCCGCGTAGGTCCGCCAATTGGGT  
 GCACCGAGAGCCGGATCGACCCCGGGGTGTCTGGGGGCCGATCCAGCGCGTTAAACCA  
  
 361 LysValIleAspThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuVal  
 AAGTCATCGATACCTTACGTGCGGCTTCGCCGACCTCATGGGTACATACCGCTCGTC  
 TTCCAGTAGCTATGGGAATGCACGCCGAAGCGCTGAGTACCCCATGTATGGCGAGCAG  
  
 421 GlyAlaProLeuGlyGlyAlaAlaArgAlaLeuAlaHisGlyValArgValLeuGluAsp  
 GCGGCCCCCTTTGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGAC  
 CCGCGGGAGAACCTCCGCGACGGTCCCGGGAACCGGTACCGCAGGCCCAAGACCTTCTG



# FIG. 72C

481 GLyValAsnTyrAlaThrGLyAsnLeuProGLyCysSerPheSerIlePheLeuLeuAla  
 GCGGTGAACtATGCAACAGGGAACCTTCCTGGTGTCTTCTCTATCTTCCTCTGGCC  
 CCGCACTTGATACGTGTGTCCTTGGAAGGACCACAGAGAAGAGATAGAAGAACCCGG

541 LeuLeuSerCysLeuThrValProAlaSerAlaTyrGlnValArgAsnSerThrGlyLeu  
 CTGCTCTCTTGTGCTTGACTGTGCCCTTCGGCTTACCAGTGCGCACTCCACGGGCTT  
 GACGAGAGAACGAACtGACACGGGCGAAGCCGGATGTTCAcCGCTTGAGGTGCCCGAA

601 TyrHisValThrAsnAspCysProAsnSerSerIleValTyrGlnAlaAlaAspAlaIle  
 TACCACGTCACCAATGATGCCCCTAACtCGAGTATGTGTACGAGCGCGCCGATGCCATC  
 ATGGTGCACTGGTTACTTAACGGGATTGAGCTCATATACACATGCTCCCGGCTACGGTAG

661 LeuHisThrProGLyCysValProCysValArgGlnGlyAsnAlaSerArgCysTrpVal  
 CTGCACACTCCGGGGTGGTCCCTTGCGTTCGTGAGGGCAACGCCCTCGAGGTGTGGTG  
 GACGTGTGAGGCCCCACGCAAGGGAACGCAAGCACTCCCGTTGCGGAGCTCCACAACCCAC

721 AlaMetThrProThrValAlaThrArgAspGlyLysLeuProAlaThrGlnLeuArgArg  
 GCGATGACCCCTACGGGTGGCCACCAAGGATGGCAAACTCCCGCGACGCACTTCGACGT  
 CGCTACTGGGATGCCACCGGTGTCCCTACCGTTTGAGGGGGCGCTGCGTCAAGCTGCA

781 HisIleAspLeuLeuValGlySerAlaThrLeuCysSerAlaLeuTyrValGlyAspLeu  
 CACATCGATCTGCTGTGTCGGGAGCGCCACCCCTGTTCGGCCCTTACGTGGGGACCTG  
 GTGTAGCTAGACGAACAGCCCTCGCGGTGGGAGACAAAGCCGGGAGATGCACCCCTGGAC

841 CysGlySerValPheLeuValGlyGlnLeuPheThrPheSerProArgArgHisTrpThr  
 TGGGGGTCTGTCTTCTGTGCGGCCAACTGTTCACCTTCTCTCCAGGGCCCACTGAGC  
 ACGCCCAAGACAGAAAGAACAGCCGGTTGACAAGTGGAAGAGAGGTCCGGGTGACCTGC



# FIG. 72D

901 ThrGlnGlyCysAsnCysSerIleTyrProGlyHisIleThrGlyHisArgMetAlaTrp  
 ACCGCAAGGTGCAATTGCTCTATCTATCCCGCCATATACGGGTCACCGCATGGCATGG  
 TGGGTTCCAACGTTAACGAGATAGATAGGGCCGGTATATTGCCAGTGGCGTACCCTACC

961 AspMetMetMetAsnTrpSerProThrThrAlaLeuValMetAlaGlnLeuLeuArgIle  
 GATATGATGATGAACGTGGTCCCTACGACGGCGTGGTAATGGCTCAGCTGCTCCGGATC  
 CTATACTACTACTTGGACCAGGGGATGCTGCCGCAACCATTTACCAGAGTCGACGAGGCCCTAG

1021 ProGlnAlaIleLeuAspMetIleAlaGlyAlaHisTrpGlyValLeuAlaGlyIleAla  
 CCACAAGCCATCTTGGACATGATCGCTGGTGTCTCACTGGGAGTCCTGCGGGCATAGCG  
 GGTGTTCCGTTAGAACCTGTACTAGCGAACCAAGAGTGACCCCTCAGGACCGCCCGTATCGC

1081 TyrPheSerMetValGlyAsnTrpAlaLysValLeuValLeuLeuLeuPheAlaGly  
 TATTCTCCATGGTGGGGAACCTGGCGAAGTCCCTGTAAGTGTGCTGCTATTGGCCGCC  
 ATAAAGAGGTACCACCCCTTGACCCGCTTCCAGGACCATCACGACGACGATAAACGGCCG

1141 ValAspAlaGluThrHisValThrGlyGlySerAlaGlyHisThrValSerGlyPheVal  
 GTCGACGGCGGAACCCACGTCACCGGGGAAGTGGCCGCCACACTGTGTCTGGATTGTGT  
 CAGCTGCGCCTTTGGGTGCAGTGGCCCCCTTCACGGCGCCGGTGTGACACAGAACCTAAACAA

1201 SerLeuLeuAlaProGlyAlaLysGlnAsnValGlnLeuIleAsnThrAsnGlySerTrp  
 AGCCTCCTCGCACCAAGCGCCAGCAGAACGTCACGCTGATCAACACCAACGCGCAGTTGG  
 TCGGAGGAGCGTGGTCCCGCGTTCGTCGTGACAGGTGCACTAGTTGTGTGTCGCCGTCACAC





# FIG. 72E

1261 HisLeuAsnSerThrAlaLeuAsnCysAsnAspSerLeuAsnThrGlyTrpLeuAlaGly  
 CACCTCAATAGCAGCGCCCTGAACTGCAATGATAGCCTCAACACCGCGCTGGCAGGG  
 GTGGAGTTATCGTGCCGGGACTTGACGTTACTATCGGAGTTGTGGCCGACCAACCGTCCC  
 1321 LeuPheTyrHisHisLysPheAsnSerSerGlyCysProGluArgLeuAlaSerCysArg  
 CTTTCTATCAACCAAGTTCAACTCTTCAGGCTGTCTGAGAGGCTAGCCAGCTGCCGA  
 GAAAGATAGTGGTGTTCAGTTGAGAAGTCCGACAGGACTCTCCGATCGGTGACGGCT  
 1381 ProLeuThrAspPheAspGlnGlyTrpGlyProIleSerTyrAlaAsnGlySerGlyPro  
 CCCCTTACCGATTTTGACCAGGGCTGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCC  
 GGGGAATGGCTAAAACTGGTCCCGACCCCGGATAGTCAATACGGTTGCCCTTCCCGGGG  
 1441 AspGlnArgProTyrCysTrpHisTyrProProLysProCysGlyIleValProAlaLys  
 GACCAGCGCCCTACTGCTGGCACTACCCCAAAACCTTGCGGTATTGTGCCCGGAAG  
 CTGTCGCGGGGATGACGACCGGTGATGGGGGTTTGGAAACGCCATATAACAGGGCGCTTC  
 1501 SerValCysGlyProValTyrCysPheThrProSerProValValGlyThrThrAsp  
 AGTGTGTGTGCTCCGGTATATTTGCTTCACCTCCAGCCCCGTGTGTGGGAACGACCGAC  
 TCACACACACCAAGGCCATATAACGAAGTGAGGCTCGGGGCAACCAACCTTGTGCTGCTG  
 1561 ArgSerGlyAlaProThrTyrSerTrpGlyGluAsnAspThrAspValPheValLeuAsn  
 AGGTGGGGCGGCCCACTACAGCTGGGGTGAATAATGATACGACGCTTTCGTCCTTAAC  
 TCCAGCCCCGCGGGGTGATGTGACCCCACTTTACTATGCTGACAGAGCAGGAATTG



FIG. 72F

1621 AsnThrArgProProLeuGlyAsnTrpPheGlyCysThrTrpMetAsnSerThrGlyPhe  
 AATACCAGGCCACCGCTGGCAATTGGTTGGTTGTTACCTGATGAACCTCACTGATTC  
 TTATGGTCCGGTGGCGACCCGTTAACCAAGCCAACATGACCTACTTGAGTTGACCTAAG  
 1681 ThrIysValCysGlyAlaProProCysValIleGlyGlyAlaGlyAsnAsnThrLeuHis  
 ACCAAAGTGTGGAGCGCCCTTGTGTCATCGGAGGGCGGGCAACACACCCCTGCAC  
 TGGTTTCACACGCCCTCGCGGAGGAACACAGTAGCCCTCCCCCGCTTGTGTGGACGTG  
 1741 CysProThrAspCysPheArgLysHisProAspAlaThrTyrSerArgCysGlySerGly  
 TGCCCCACTGATGCTTCGCAAGCATCCGGACGCCACATACTCTCGGTGGCTCCGCT  
 ACGGGGTGACTAACGAAGCGCTTCGTAGGCCCTGGCGGTGTATGAGGCCACGCCGAGGCCA  
 1801 ProTrpLeuThrProArgCysLeuValAspTyrProTyrArgLeuTrpHisTyrProCys  
 CCTGGATCACACCCAGGTGCCCTGCTGCATACCCGTATAGCCTTGGCATTATCCTGT  
 GGGACCTAGTGTGGTCCACGGACCGACTGATGGGCATATCCGAAACCGTAATAGGAACA  
 1861 ThrIleAsnTyrThrIlePheLysIleArgMetTyrValGlyGlyValGluHisArgLeu  
 ACCATCAACTACACCATATTTAAATCAGGATGTACGTGGAGGGGTGAAACACAGGCTG  
 TGGTAGTTGATGTGGTATAAATTTAGTCTACATGCACCCCTCCAGCTTGTGTCCGAC  
 1921 GluAlaAlaCysAsnTrpThrArgGlyGluArgCysAspLeuGluAspArgAspArgSer  
 GAAGCTGCCCTGCAACTGACGCGGGCGAACGTTGCGATCTGAAGACAGGACAGGTCC  
 CTTGACGGACGTTGACCTGCGCCCGCTTGCAACGCTAGACCTTCTGTCCCTGTCCAGG  
 1981 GluLeuSerProLeuLeuLeuThrThrGlnTrpGlnValLeuProCysSerPheThr  
 GAGCTCAGCCCCGTTACTGCTGACCACTACACAGTGGCAGGTCCCTCCGTCTTCTCACA  
 CTCGAGTCGGGCAATGACGACTGGTGATGTGTACCCGTCCAGGAGGGCACAAAGGAAGTGT



# FIG. 72G

2041 ThrLeuProAlaLeuSerThrGlyLeuIleHisLeuHisGlnAsnIleValAspValGln  
ACCCATACCAGCCTTGTCCACCGGCTCATCCACCCTCCACGACATTTGGACGTGCAG  
TGGGATGGTCCGAACAGGTGGCCCGAGTAGGTGGAGGTGGTCTTGTAAACACCTGCACGTC

2101 TyrLeuTyrGlyValGlySerSerIleAlaSerTrpAlaIleLysTrpGluTyrValVal  
TACTTGTACGGGGTGGGGTCAAGCATCGCGTCTGGGCCATTAACTGGAGTACGTCGTT  
ATGAACATGCCCCACCCCAAGTTCTGTAGCCGACGACCCGGTAAATTCAACCTCATGCACCAA

2161 LeuLeuPheLeuLeuLeuAlaAspAlaArgValCysSerCysLeuTrpMetMetLeuLeu  
CTCCTGTTCCTTCTGCTTGACAGACGCGCGCTCTGCTCTGCTTGTGATGATGCTACTC  
GAGGACAAGGAAGACGAACGTCTGCGCGCGCAGACGAGACGAACACCTACTACGATGAG

2221 IleSerGlnAlaGluAlaAlaLeuGluAsnLeuValIleLeuAsnAlaAlaSerLeuAla  
ATATCCCAAGCGAGCGCGCTTTGGAGAACCTCGTAATACTTAATGCAGCATCCCTGGCC  
TATAGGGTTGCGCTCCGCCGAACCTCTTGGAGCATTAATGAATTACGTCGTAGGGACCGG

2281 GlyThrHisGlyLeuValSerPheLeuValPhePheCysPheAlaTrpTyrLeuLysGly  
GGGACGCACGGTCTGTATCCCTTCCTGCTGTTCTTCTTGCATGGTATTGAAGGT  
CCCTGCCGTGCCAGAACATAGGAAGGACGACACAGAAGACGAACGTACCATAACTTCCA

2341 LysTrpValProGlyAlaValTyrThrPheTyrGlyMetTrpProLeuLeuLeuLeu  
AAGTGGGTGCCCGAGCGGTCTACACCTTCTACGGGATGTGCCCTCTCCTGCTCCTG  
TTCACCCACGGGCTCGCCAGATGTGAAGATGCCCTACACCGGAGAGGAGACGAGGAC

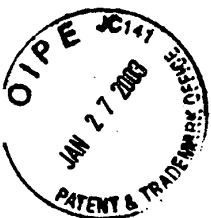


FIG. 72H

2401 LeuAlaLeuProGlnArgAlaTyrAlaLeuAspThrGluValAlaAlaSerCysGlyGly  
TTGGCGTTGCCCGACGGGGCGTACGGCTGGACACGAGGTGGCCGCTGTTGGCGGT  
AACCGCAACGGGGTCCGCCCATGGCGAACCTGTGCCCTCCACCGGGCAGCACACCGCCA  
2461 ValValLeuValGlyLeuMetAlaLeuThrLeuSerProTyrTyrIleSer  
GTTGTTCTCGTCGGGTGATGGCGCTGACTCTGTCAACCATATTACAGCGCTATATCAGC  
CAACAAGAGCAGCCCACTACCGGACTGAGACAGTGGTATATGTTCGGCATATAGTCCG  
2521 TrpCysLeuTrpTrpLeuGlnTyrPheLeuThrArgValGluAlaGlnLeuHisValTrp  
TGGTGCTTGTGGTGGCTTCAGTATTTTCTGACCAGAGTGAAGCGCACTGCACGTGG  
ACCACGAACACCAACCGAAGTCAATAAAGACTGGTCTCACCTTCCGCTTGACGTGCACACC  
2581 IleProProLeuAsnValArgGlyGlyArgAspAlaValIleLeuLeuMetCysAlaVal  
ATTCCCCCCTCAACGTCGAGGGGGCGCGGACGCCGTCATCTTACTCATGTGTGTGTA  
TAAGGGGGGAGTTGCAGGCTCCCCCGGCTGCGGAGTAGAATGAGTACACACGACAT  
2641 HisProThrLeuValPheAspIleThrIleLeuLeuAlaValPheGlyProLeuTrp  
CACCCGACTCTGGTATTGACATCACCAATTTGCTGTGGCCGCTTCGACCCCTTTGG  
GTGGGCTGAGACCATAAACTGTAGTGTTAACGACGACCGGCAGAACCTGGGGAACC  
2701 IleLeuGlnAlaSerLeuLeuLysValProTyrPheValArgValGlnGlyLeuLeuArg  
ATTCTTCAAGCCAGTTTGTCTTAAAGTACCCTACTTTGTGGCGGTCCAGGCCCTTCTCCGG  
TAAGAAGTTCGGTCAACGAATTTTCATGGGATGAACAACGCGCAGGTTCCGGAAGAGGCC



# FIG. 721

2761 pheCysAlaLeuAlaArgLysMetIleGlyGlyHisTyrValGlnMetValIleIleLys  
 TTCCTGCGCGTTAGCGCGGAGAGATGATCGAGGCCATTACGTGCAATGTGCATCATTAAG  
 AAGACGCGCAATCGCGCCTTCTACTAGCCTCCGGTAATGCACGTTTACCAGTAGTAATTCTC  
 2821 LeuGlyAlaLeuThrGlyThrTyrValTyrAsnHisLeuThrProLeuArgAspTrpAla  
 TTAGGGCGGCTTACTGGCACCTATGTTTATAACCATCTCACTCCTCTTCGGGACTGGCGG  
 AATCCCCCGCAATGACCGGTGATACAAATATTGGTAGAGTGAGAGAGAAGCCCTGACCCCGC  
 2881 HisAsnGlyLeuArgAspLeuAlaValAlaValGluProValValPheSerGlnMetGlu  
 CACACGCGCTTGGAGATCTGGCCGTGCTGTAGAGCCAGTCGCTTCTCCCAATGGAG  
 GTGTTGCCGAACGCTCTAGACCGGCACCGACATCTCGGTCAGCAGAAGAGGTTTACCCTC  
 2941 ThrLysLeuIleThrTrpGlyAlaAspThrAlaAlaCysGlyAspIleIleAsnGlyLeu  
 ACCAAGCTCATCACGTGGGGGGCAGATACCGCCGCTGCGGTGACATCATCAACGGCTTG  
 TGGTTCGAGTAGTGCACCCCGCTCTATGGCGGGCAGCCGCACTGTAGTAGTTGCCGAAC  
 3001 ProValSerAlaArgArgGlyArgGluIleLeuLeuGlyProAlaAspGlyMetValSer  
 CCTGTTTCCGCCCCGAGGGCGCGGAGATACTGCTCGGGCCAGCCGATGGAATGCTCTCC  
 GGACAAAGCGGGCGCTCCCGCCCTCTATGACGAGCCCGGTGCGCTTACCAGAGG  
 3061 LysGlyTrpArgLeuLeuAlaProIleThrAlaTyrAlaGlnGlnThrArgGlyLeuLeu  
 AAGGGGTGAGGTTGCTGCGCGCCCATCACGGCGTACGCCCAGCAGACAAAGGGGCTCCTA  
 TTCCCCACCTCCAAACGACCGGGTAGTGCAGCATGCGGGTCTGTTTCCCGGAGGAT  
 3121 GlyCysIleIleThrSerLeuThrGlyArgAspLysAsnGlnValGluGlyGluValGln  
 GGGTGCAATAACACCGAGCTAAGTGGCGGCAAAACCAAGTGAGGGTGAGGTTCCAG  
 CCCACGTATTAGTGGTGGATTGACCGGCCCTGTTTGTGTTTCACTCCCACTCCAGGTC



# FIG. 72J

3181 ILeValSerThrAlaIaGlnThrPheLeuAlaThrCysIleAsnGlyValCysTrpThr  
 ATGTGTCAACTGCTGCCAAACCTTCTCGGCAACGTGCATCATGGGTGTGCTGACT  
 TAACACAGTTGACGACGGGTTTGAAAGGACCGTTGCACGTAGTTACCCACACGACCTGA  
  
 3241 ValTyrHisGlyAlaGlyThrArgThrIleAlaSerProLysGlyProValIleGlnMet  
 GTCTACCAACGGGGCCGGAACGAGGACCATCGCGTCACCCAAAGGTCCTGTCAATCCAGATG  
 CAGATGGTGCCCGGCGCTTGCTCTGTTAGCGCAGTGGGTTCCAGAGACAGTAGGTCTTAC  
  
 3301 TyrThrAsnValAspGlnAspLeuValGlyTrpProAlaProGlnGlySerArgSerLeu  
 TATACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCCGCAAGGTAGCCGCTCATTTG  
 ATATGGTTACATCTGGTTCTGGAACACCCGACCGGGCGAGCGTTCCATCGCGGAGTAAC  
  
 3361 ThrProCysThrCysGlySerSerAspLeuTyrLeuValThrArgHisAlaAspValIle  
 ACACCCCTGCACCTTGGCGCTCTCGGACCTTACCTGTGTCACGAGCACGCCGATGTCAATT  
 TGTGGACGTGAACGCCGAGGACCTGGAATGACCAAGTGTCTCCGTGCGGCTACAGTTAA  
  
 3421 ProValArgArgArgGlyAspSerArgGlySerLeuLeuSerProArgProIleSerTyr  
 CCCGTGCGCGCGGGGGGTGATAGCAGGGGCAGCCTGTGTCGCCCGGCCCATTTCCCTAC  
 GGGCACGCGGGCGGCCCACTATCGTCCCGTGGACGACAGCGGGCGCGGTAAAGGATG  
  
 3481 LeuLysGlySerSerGlyGlyProLeuLeuCysProAlaGlyHisAlaValGlyIlePhe  
 TTGAAGAAGCTCTCGGGGGGTCCGCTGTGTGCCCGCGGGGCACGCCGTGGCATATTT  
 AACTTTCCGAGGAGCCCCCAGCGCACACACGGGGCGCCCCGTGCGGCACCCGTATATAA  
  
 3541 ArgAlaAlaValCysThrArgGlyValAlaLysAlaValAspPheIleProValGluAsn  
 AGGGCGCGGTGTGCACCCGTGAGTGCTAAGGCGGTGACCTTATCCCTGTGAGAAAC  
 TCCCGGCGCACACGTGGGCACCTCACCGATTCCGCCACCTGAATAATAGGACACCTCTTG

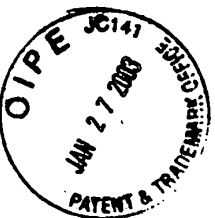


FIG. 72K

3601 LeuGIuThrThrMetArgSerProValPheThrAspAsnSerSerProProValValPro  
CTAGAGACACACCATGAGTCCCGGTTCACGAGTAATCTCTCCACAGTAGTGCCC  
GATCTCTGTGTGTA CTCCAGGGGCCACAAGTGCCTATTGAGAGAGAGGTGTCATCACGGG  
3661 GlnSerPheGlnValAlaHisLeuHisAlaProThrGlySerGlyLysSerThrLysVal  
CAGAGCTTCCAGGTGGCTCACCCTCATGCTCCACAGGCGAGCGGCAAAAGCACCAAGGC  
GTCTCGAAGGTCCACCGAGTGGAGGTACGAGGGTGTCCGCTTTCGTTCCAG  
3721 ProAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsnProSerValAlaAla  
CCGGCTGCATATGCAGCTCAGGCTATAGTGCTAGTACTCAACCCCTGTGCTGCA  
GGCCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAGTTGGGAGACAACGACGT  
3781 ThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAspProAsnIleArgThr  
ACACTGGGCTTGGTGTCTTACATGTCAGGCTCATGGGATCGATCTTACATCAGGACC  
TGTGACCCGAACCAACGAATGTACAGGTTCCGAGTACCCTAGCTAGGATTGTAGTTCCTGG  
3841 GlyValArgThrIleThrThrGlySerProIleThrTyrSerThrTyrGlyLysPheLeu  
GGGCTGAGAACATTTACCACTGGCAGCCCCCATCAGTACTCCACCTACGGCAAGTTCCTT  
CCCCACTCTTGTTAATGTGACCGCTCGGGGTAGTGCATGAGGTGATGCCGTTCAAGGAA  
3901 AlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCysAspGluCysHisSer  
GCCGACGGCGGGTGTCTCGGGGGGGCTTATGACATATAATTTGTGACGAGTGCCACTCC  
CGGCTGCCGCCACGAGCCCCCGGCAATACTGTATTATTAAACACTGCTCAGCGTGAGG

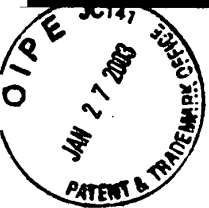
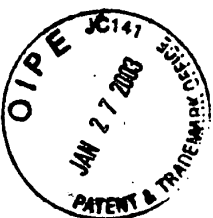


FIG. 72L

3961 ThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGlnAlaGluThrAlaGly  
ACGGATGCCACATCCATCTTGGCATCGCACTGCTTGAACAAGCAGAGACTGGGGG  
TGCCTACGGGTAGGTAGAACCCTAGCCGTACAGGAACCTGTTGTTCTCTGACGCCCC  
4021 AlaArgLeuValValLeuAlaThrAlaThrProProGlySerValThrValProHisPro  
GGGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTCACTGTGCCCATCCC  
CGCTCTGACCAACACGAGCGGTGGCGGTGGGAGGCCCGAGGCAGTGACACGGGGTAGGG  
4081 AsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPheTyrGlyLysAlaIle  
AACATCGAGGAGGTGCTCTGTCCACCAACCGAGAGATCCCTTTTACGGCAAGGCTATC  
TTGTAGCTCCCTCCAACGAGACAGGTGGTGGCTCTCTAGGGAATAATGCCGTTCCGATAG  
4141 ProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHisSerLysLysCys  
CCCCTCGAAGTAATCAAGGGGGGAGACATCTCATCTTCTGTCATTCAAGAAGAGTGC  
GGGAGCTTCATTAGTTCCCCCCCCCTCTGTAGAGTAGAAGACAGTAAGTTCTTCTTCACG  
4201 AspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaValAlaTyrTyrArgGly  
GACGAACCTGCCCGCAAGCTGTGTCATTTGGCATCAATGCCGTGGCTTACTACCGCGGT  
CTGCTTGAGCGCGTTTCGACCAGCGTAACCCGTAGTTACGGCACCGGATGATGGCCCA  
4261 LeuAspValSerValIleProThrSerGlyAspValValValAlaThrAspAlaLeu  
CTTGACGTGTCCGTCAATCCCGACCAAGCGCGCATGTTGTGTCGTGGCAACCGATGCCCTC  
GAACTCACACAGGCAAGTAGGGCTGGTGGCGCTACACACAGCACACCGTTGGCTACGGGAG





# FIG. 72M

4321 MetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsnThrCysValThrGln  
ATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCATATACGTGTGCACCCAG  
TACTGGCCGATATGGCCCGCTGAAGCTGAGCCACTATCTGACGTATATGCACACAGTGGGTC

4381 ThrValAspPheSerLeuAspProThrPheThrIleGluThrIleThrLeuProGlnAsp  
ACAGTCGATTTCAGCCTTGACCTTACCCTTACCATTGACATCAACATCAGCCTCCCCAGGAT  
TGTCAAGCTAAAGTCGGAACCTGGGATGGAGTGTAACCTCTGTAGTGGAGGGGCTCCTA

4441 AlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLysProGlyIleTyrArg  
GCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAGCCAGGCATCTACAGA  
CGACAGAGGGCGGTGAGTTGCAGCCCCGCTCCTGACCGTCCCCCTTCGGTCCGTAGATGTCT

4501 PheValAlaProGlyGluArgProSerGlyMetPheAspSerSerValLeuCysGluCys  
TTTGTGGCACCGGGGAGCGCCCTCCGGCATGTTCGACTGCTCCGTCTGTGAGTGC  
AAACACCGTGGCCCCCTCGCGGGGAGCGGTACAAAGCTGAGCAGGCAGAGACACTCACG

4561 TyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThrThrValArgLeuArg  
TATGACGCGAGGCTGTGCTGTGATGAGCTCACGCCCGCCGAGACTACAGTTAGGCTACGA  
ATACTGCGTCCGACACGAACCATATCTGAGTGGCGGGGCTCTGATGTCAATCCGATGCT

4621 AlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeuGluPheTrpGluGly  
GCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTTGAATTTTGGGAGGGC  
CGCATGTACTTGTGGGGCCCCGGAAGGGCACACGGTCTCTGTAGAACTTAAAAACCTTCCCG

4681 ValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGlnThrLysGlnSerGly  
GTCTTTACAGGCGCTCACTCATATAGATGCCCACTTTCTATCCAGACAAAGCAGAGTGGG  
CAGAAATGTCCGGAGTGAATATATCTACGGGTGAAGATAGGGTCTGTTCGCTCAACCC



FIG. 72N

4741 GluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAlaArgAlaGlnAlaPro  
 GAGAACCTTCCCTTACCTGGTAGCGGTACCAGCCACCGGTGCGCTAGGGCTCAAGCCCT  
 CTCTTGGAAGGAATGGACCATCGCATGGTTCCGGTGGCACACCGCATCCGAGTTCGGGGA  
  
 4801 ProProSerTyrPaspGlnMetTrrPlyScysLeuIleArgLeuLysProThrLeuHisGly  
 CCCCCTATCGTGGGACAGATGTGGAAGTGTGATTGCTCAAGCCACCCCTCATGGG  
 GGGGTAGCACCCCTGGTCTACACCTTCACAACCTAAGCGGAGTTCGGGTGGAGGTACCC  
  
 4861 ProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIleThrLeuThrHisPro  
 CCAACACCCCTGCTATACAGACTGGCGCTGTTCAGAAAGAAATCACCCCTGACGACCCCA  
 GGTGTGGGACGATATGTCTGACCCCGACAAAGTCTTACTTTAGTGGGACTGCGTGGGT  
  
 4921 ValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluValValThrSerThrTyr  
 GTCACCAAAATACATCATGACATGATGTCGGCCGACCTGGAGGTGCTACGAGCACCTGG  
 CAGTGGTTATGTAGTACTGTACTGACGACCCGGCTGGACCTCCAGCAGTGTCTGTGACC  
  
 4981 ValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeuSerThrGlyCysVal  
 GTGCTCGTTGGCGGCGCTCGCTGGCTTTGGCCGCGGTATTGCTGTCAACAGGCTGCGTG  
 CACGAGCAACCGCGCCGACGAGACCGAAACCGCGCATTAACGGACAGTTGTCCGACGCAC  
  
 5041 ValIleValGlyArgValValLeuSerGlyLysProAlaIleIleProAspArgGluVal  
 GTCATAGTGGGACAGGCTCGTCTGTCCGGAAGCCGCAATCATATACCTGACAGGAAATC  
 CAGTATCACCCCGTCCACAGCAGAACAGGCCCTTCGGCCGTTAGTATGACTGTCCCTTCAG  
  
 5101 LeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeuProTyrIleGluGln  
 CTCTACCGAGAGTTTCGATGAGATGGAAGAGTGTCTTCAGCAGCACTTACCGTACATCGACAA  
 GAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTGTGAATGGCATGTAGCTCGTT

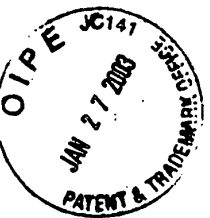


FIG. 720

5161 GlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSer  
GGGATGATGCTCGCCGAGCAGTTCAAGCAGAGGCCCTCGGCCCTCCAGACCGCGTCC  
CCCTACTACGAGCGGCTCGTCAAGTTCGTTCCGGGAGCCGGAGGACGTCTGGCCGACAG

5221 ArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGlnLysLeuGluThrPhe  
CGTCAGGCAGAGGTTATCGCCCTGCTGTCAGACCACTGGCAAAACTGAGACCTTC  
GCAGTCCGTCCTCCAATAGCGGGGACGACAGGTCGTGTTGACCGTTTGTGAGCTCTGGAAG

5281 TrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeuAlaGlyLeuSerThr  
TGGCGAAGCATATGTGAACTTCATCAGTGGGATACAAATACCTGGCGGCTTGTCACG  
ACCCGCTTCGTATACACCTTGAAGTAGTCACCCCTATGTTATGAACCGCCCGAACAGTTGC

5341 LeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAlaAlaValThrSerPro  
CTGCCCTGGTAACCCCGCCCATTTGCTTCAATGATGGCTTTTACAGCTGCTGTACACCGCCA  
GACGGAACCATTTGGGGCGGTAAACGAAGTAACCTACCGAAATGTGACGACGACGAGTGGGT

5401 LeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrpValAlaAlaGlnLeu  
CTAACCACTAGCCAAACCCCTCCTTCAACATATTTGGGGGGGTGGGTGGCTGCCACAGCTC  
GATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCACCCACCGACGGGTGAG

5461 AlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAlaGlyAlaAlaIleGly  
GCCGCCCGCGGTGCGCTACTGCCCTTGTGGCGCGCTGCTAGCTGGCGCCGACATCGGC  
CGCGGGGGCCACGGCGATGACGGAACAACCCGACCGAATCGACCGCGGTAGCCG

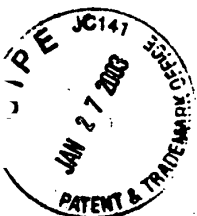
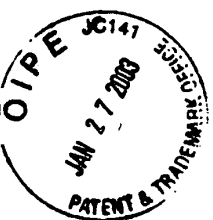


FIG. 72P

5521 SerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyrGlyAlaGlyValAla  
AGTGTGGACTGGGGAAGTCCATAGACATCCTTGCAGGGTATGGCGGGCGTGGCG  
TCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATACCGCGCCGCCACCGC  
5581 GlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSerThrGluAspLeuVal  
GGAGCTCTTGTGGCATTCAGATCATGAGCGGTGAGGTCCCTCCACGGAGACCTGGTC  
CCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGGTGCCCTCTGGACCAG  
5641 AsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGlyValValCysAlaAla  
AATCTACTGCCCCGCCATCTCTCGCCGGAGCCCTCGTAGTCGGCGTGTCTGTGCAGCA  
TTAGATGACGGGGCGGTAGGAGAGCGGCCCTCGGAGCATCAGCCGACCAAGACACGTCTGT  
5701 IleLeuArgArgHisValGlyProGlyGluGlyAlaValAlaGlnTrpMetAsnArgLeuIle  
ATACTGCGCGCGGCACGTTGGCCCCGGCGAGGGGGCAGTGCAGTGAATGAACCGGCTGATA  
TATGACGGGGCGGTGC AACCGGGGCCGCTCCCGGTCACTGTAACCTACTTGGCCGACTAT  
5761 AlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrValProGluSerAspAla  
GCCCTTGGCTCCCGGGGAACCATGTTTCCCCACGCACTACGTGCCGAGAGCGATGCA  
CGGAAGCGGAGGGCCCCCTTGTGTACAAAGGGGTGCGTGATGCACGGCCCTCTGCTACGT  
5821 AlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGlnLeuLeuArgArgLeu  
GCTGCCCCGCGTCACTGCCATATCATGACGAGCCTCACTGTAACCCAGCTCTGAGGCGACTG  
CGACGGGGCGCAGTGACGGTATGAGTCTGCGAGTGACATTTGGGTGAGGAGCTCCGCTGAC



# FIG. 72Q

5881 HlsglnTrpIleSerSerGluCysThrThrProCysSerGlySerTrpLeuArgAspIle  
CACCAGTGGATAGCTCGAGGTGTAACCACTCCATGCTCCGGTTCTGCTAAGGACATC  
GTGGTCACCTATTTCGAGCCTCACATGGTGAAGTACGAGGCCAAGACCATTCCCTGTAG  
5941 TrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeuLysAlaLysLeuMet  
TGGACTGGATATGCGAGGTGTGAGCGACTTTAAGACCTGGCTAAAGCTAAGCTCATG  
ACCCTGACCTATACGCTCCACAACCTGCTGAAATTCTGGAACCGATTTTTCGATTTCGAGTAC  
6001 ProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyrLysGlyValTrpArg  
CCACAGCTGCCCTGGGATCCCTTTGTGTCTGCTGCCAGCGCGGTATAGGGGCTCGCGA  
GGTGTGACGGACCCCTAGGGGAACACAGGACGGTCCGCCCATATTCCCCAGACCGCT  
6061 ValAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIleThrGlyHisValLys  
GTGACGCGCATCATGCACACTCGCTGCCACTGTGAGCTGAGATCACTGCACATGTCAAA  
CACCTGCCGTAGTAGGTGTGAGCGACGGTGACACCTCGACTCTAGTGACCTGTACAGTTT  
6121 AsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMetTrpSerGlyThrPhe  
AACGGACGATGAGGATCGTGGTCTAGGACCTGCAGACATGTGAGTGGACCTTC  
TTGCCCTGCTACTCCTAGCAGCCAGGATCCTGAGACGTCTTGTACACCTCACCCCTGAAG  
6181 ProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAlaProAsnTyrThrPhe  
CCCATTAATGCCTACACACGCGGCCCTGTACCCCTTCCTGCGCCGAACATACACGTTTC  
GGGTAATTACGGATGTGTGCCCGGGGACATGGGGGAAGAGACGCGGCTTGATGTGCAAG

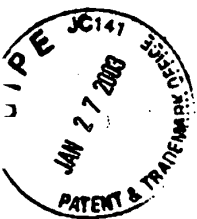


FIG. 72R

6241 AlaleuTrpargValSerAlaglUglUtyrValGluIleargGlnValGlyaspPheHis  
GCGCTATGAGGGTGTCTGCAGAGGAATATGTGAGATAAGCAGGTGGGGACTTCAC  
CGCGATACCTCCACAGACGTCTCCTATACACCTCTATTCCGTCCACCCCTGAAGGTG

6301 TyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGlnValProSerProGlu  
TACGTGACGGGTATGACTACTGACAATCTCAATGCCCCGTGCCAGGTCCCATGCCCGAA  
ATGCACCTGCCCATACTGATGACTGTAGAGTTTACGGGCACGGTCCAGGGTAGCGGGCTT

6361 PhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaProProCysLysProLeu  
TTTTTACAGAAATTGACGGGGTGGCTTACATAGGTTTGGCCCCCTGCAAGCCCTTG  
AAAAAGTGTCTTAACTGCCCCCAGCGGATGTATCCAAACGCGGGGACGTTCCGGAAAC

6421 LeuArgGluGluValSerPheArgValGlyLeuHisGlyUtyrProValGlySerGlnLeu  
CTGCGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCGGTAGGGTCGCAATT  
GACGCCCTCCTCCATAGTAAGTCTCATCTGAGGTGCTTATGGGCCATCCACGCTTAAT

6481 ProCysGluProGluProAspValAlaValLeuThrSerMetLeuThrAspProSerHis  
CCTTGGAGCCCCGAACCGGACGTGGCCGTGTGACGTCCATGCTCAGTATCCCTCCCAT  
GGAACGCTCGGGCTTGGCCCTGCACCGGCACAACCTGACGTAAGTACAGGAGGTA

6541 IleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerProProSerValAlaSer  
ATAACAGCAGAGCGCGCGCGGAAGGTTGGCGAGGGGATCACCCCTCTGTGGCCAGC  
TATTGTCTCTCCGCGCGCCGCTTCCAACCGCTCCCTAGTGGGGGAGACACCGGTCG

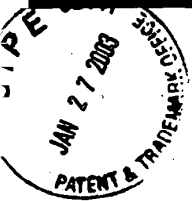
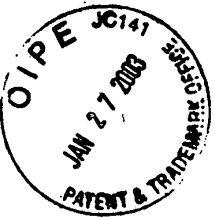


FIG. 72S

6601 SerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCysThrAlaAsnHisAsp  
TCCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCACTTGCAACCGCTAACCATGAC  
AGGAGCCGATCGGTCGATAGCGGAGGTAGAGAGTCCGTTGAACGTGGCATTTGTTACTG  
6661 SerProAspAlaGlnLeuIleGlnAlaAsnLeuLeuTrpArgGlnGlnMetGlyGlyAsn  
TCCCTGTAGCTGAGCTCATAGAGGCCAACCTCTTATGAGGACAGAGATGGCGGCAAC  
AGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTTCTTACCCCGCTTG  
6721 IleThrArgValGlnSerGlnAsnLysValIleLeuAspSerPheAspProLeuVal  
ATCACCCAGGTTGAGTCAGAAACAAGTGTGATTTCTGACTCTTCGATCCGCTTGTG  
TAGTGGTCCCACTCAGTCTTTTGTTCACCACTAAGACCTGAGGAAGCTAGGCGAACAC  
6781 AlaGlnGluAspGlnArgGlnIleSerValProAlaGlnIleLeuArgLysSerArgArg  
GCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGACAGAAATCCTGCGAAGTCTCGAGA  
CGCTCTCTCTGCTCGCCCTCTAGAGGCATGGCGCTCTTTAGGACGCCCTTCAGAGCCTCT  
6841 PheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnProProLeuValGlnThr  
TTGCCCCAGGCCCTGCCGTTTGGCGCGCGGACTATAACCCCCCTAGTGAGACG  
AAGCGGCTCCGGGACGGGCAACCCGCGCGCTGATATTGGGGGGCGGATCACCTCTGC  
6901 TrpLysLysProAspTyrGlnProProValValHisGlyCysProLeuProProLys  
TGGAAAAAGCCCGACTACGAACCACTGTGCTCATGGCTGTCGCTTCACCTCCAAG  
ACCTTTTTCGGGCTGATGCTTGTGACACCAAGTACCGACAGCGGAAGGTGAGGTTTC  
6961 SerProProValProProArgLysLysArgThrValValLeuThrGlnUserThrLeu  
TCCCTCTCTGTGCTCTCCGCTCGAAGAAGCGGACGGTGTCTCACTGAATCAACCTA  
AGGGAGGACACGAGGCGGAGCCTTCTTCTGCTCCACCAAGAGTGACTTAGTTGGAT



# FIG. 72T

7021 SerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSerSerThrSerGlyIle  
TCTACTGCCCTTGGCCGAGCTCGCCACGAGAAGCTTTGGCAGCTCCTCAACTTCCGGCATTT  
AGATGACGGAAACCGGCTCGAGCGGTGTTCTTCGAAACCGTCGAGGAGTTGAAGGCCGTAA

7081 ThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGlyCysProProAspSer  
ACGGCGCAATATGACACACATCCTCTGAGCCCCCTCTGCTGCCGCCCGGACTCC  
TGCCCGCTGTTATGCTGTTGTAAGAGACTCGGGCGGGGAAGACCGAGCGGGGCTGAGG

7141 AspAlaGluSerTyrSerSerMetProProLeuGluGlyGluProGlyAspProAspLeu  
GACGCTGAGTCCCTATTCTCCATGCCCCCTGAGGGGAGCCTGGGATCCGGATCTT  
CTGCGACTCAGGATAAGAGGTAACGGGGGACCCTCCCCCTCGGACCCCTAGGCCCTAGAA

7201 SerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGluAspValValCysCys  
AGCGACGGGTCAATGTCACACGGTCAGTAGTGAGGCCACGCGGAGGATGTCGTGCTGC  
TCGCTGCCAGTACCAGTTCACATCACTCCGTTGCGCTCTCTACAGCACACGACG

7261 SerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAlaAlaGluGluLys  
TCAATGTCCTTACTCTTGACAGCGGCACTGTCACCCCGTGGCCGCGAAGACAGAAA  
AGTTACAGAAATGAGAACCCTGTCGCGGTGAGCAGTGGGGCACGCGGCCCTTCTGTCTTT

7321 LeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsnLeuValTyrSerThr  
CTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCAACCAATTGCTGATTTCCACC  
GACGGGTAGTTACGTGATTCTGTTGAGCAACGATGCAGTGTTGTTAAACCATATAAGGTGG

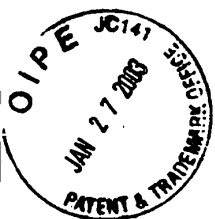




FIG. 72U

7381 ThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAspArgLeuGlnValLeu  
 ACCTCACGCGAGTGGCTTGCCCAAGGCGAGAGAAGTCACATTTGACAGACTGCAGATTCTG  
 TGGAGTGGCTCACGAACGGTTTCCGTTCTTCTTCAAGTGTAAACTGTCTGACGTTCAAGAC

7441 AspSerHisTyrGlnAspValLeuLysGlnValLysAlaAlaAlaSerLysValLysAla  
 GACAGCCATTACGAGGAGCGTACTCAAGGAGGTTAAAGCAGCGCGCTCAAAAGTGAAGGCT  
 CTGTCGGTAATGGTCCCTGCATGAGTTCTCCAATTTGCTGCCGCGCAGTTTTCACCTTCCGA

7501 AsnLeuLeuSerValGlnGluAlaCysSerLeuThrProProHisSerAlaLysSerLys  
 AACTTGCCTATCCGTAGAGGAAGCTTGCAGCCCTGACGCCCCCACACTCAGCCCAAATCCAAAG  
 TTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGGTGAGTCGGTTTAGGTTT

7561 PheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAlaValThrHisIleAsn  
 TTTGGTTATGGGGCAAAAGACGTCCTGTCATGCGCAGAAAGCGGTAAACCCACATCAAC  
 AAACCAATACCCCGTTTCTGACAGGCAACGGTACGGTCTTCCGGCATTTGGGTGAGTTTG

7621 SerValTrpLysAspLeuGlnuAspAsnValThrProIleAspThrThrIleMetAla  
 TCCGTGTGGAAGACCTTCTGGAAGACAATGTAAACACCAATAGACACTACCATCATGGCT  
 AGGCACACCTTTCTGGAAGACCTTCTGTACATTTGTGTTATCTGTGATGGTAGTACCGA

7681 LysAsnGlnuValPheCysValGlnProGlnLysGlyGlyArgLysProAlaArgLeuIle  
 AAGAACGAGGTTTCTCTGCGTTTCAGCCTGAGAAAGGGGGTCTGTAAGCCAGCTGCTCATTC  
 TTCTTGTCTCCAAAGACGCAAGTCGACTCTTCCCCCAGCATTCGGTTCAGCAGAGTAG

7741 ValPheProAspLeuGlyValArgValCysGlnLysMetAlaLeuTyrAspValValThr  
 GTGTTCCCGCATCTGGGGCGTGGCGGTGTGCGAAAGATGGCTTTGTACGACGCTGTTACA  
 CACAAGGGGCTAGACCCGCGACGCGCACACGCTTTTCTACCGAAACATGCTGCACCAATGT

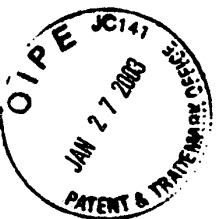


FIG. 72V

7801 LysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyrSerProGlyGlnArg  
AAGCTCCCTTGCGCGTGATGGGAAGCTCCCTACGATTCACAATACTCACCAGACAGCGG  
TTCGAGGGGAACCGGCACCTACCCTTCGAGGATGCCCTAAGGTTATGAGTGGTCCCTGTCGCC  
7861 ValGluPheLeuValGlnAlaTyrPlySerLysLysThrPrometGlyPheSerTyrAsp  
GTTGAATTCCCTCGTGCAGCGGTGAAGTCCAAGAAAACCCCAATGGGTTCTCGTATGAT  
CAACTTAAGGAGCACGTTCCGACCTTCAGGTTCTTTGGGGTTACCCCAAGACATACTA  
7921 ThrArgCysPheAspSerThrValThrGluSerAspIleArgThrGluGlnAlaIleTyr  
ACCCGCTGCTTTGACTCCACAGTCAGTGAAGCGACATCCGTACGAGAGGCAATCTAC  
TGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGCCCTCCGTTAGATG  
7981 GlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSerLeuThrGluArgLeu  
CAATGTTGTGACCTCGACCCCAAGCCCGGTGGCCATCAAGTCCCTCACCAGAGGCTT  
GTTACAACACTGAGCTGGGGTTCCGGCCACCGGTAGTTCAAGGAGTGGCTCTCCGAA  
8041 TyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnGlyTyrArgArgCysArg  
TATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGCTATCGCAGGTGCCG  
ATACAACCCCGGAGAAATGTTAGTTCCCCCTCTTGACGCCGATAGCGTCCACGGCG  
8101 AlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCysTyrIleLysAlaArg  
GCGAGCGGCGTACTGACAACTAGCTGTGTTAACACCCCTCACTTGCTACATCAAGGCCCGG  
CGCTCGCCGCATGACTGTGTGATCGACACCATTTGTGGAGTGAACGATGTAGTTCCGGGCC

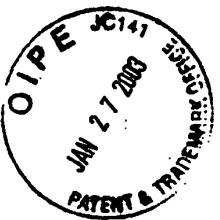


FIG. 72W

8161 AlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuValCysGlyAspAspLeu  
GCAGCCTGTGAGACCGCCAGGGCTCCAGGACTGCACCATGCTCGTGTGTGGCAGCACTTA  
CGTCGGACAGCTCGGCGTCCCGAGGTTCTGACGTGTACGAGCACACACCGCTGCTGAAT

8221 ValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSerLeuArgAlaPheThr  
GTCGTTATCTGTGAAGCGCGGGGTCCAGAGAGACGCGCGGAGCCTGAGAGCCTTCACG  
CAGCAATAGACACTTTCGCGCCCCAGGTTCTCTGCGCGCTCGGACTCTCGGAAGTGC

8281 GluAlaMetThrArgTyrSerAlaProGlyAspProGlnProGluTyrAspLeu  
GAGCTATGACCAGGTACTCCGCCCCCTGGGGACCCCCACAAACAGATACGACTTG  
CTCCGATACTGGTCCATGAGGCGGGGGGAGACCCCTGGGGGTGTGTCTTATGCTGAAC

8341 GluLeuIleThrSerCysSerSerAsnValSerValAlaHisAspGlyAlaGlyLysArg  
GAGCTCATATACATCATGCTCTCCAACGTGTCAAGTCCGCCACGACGCGCTGGAAAGAGG  
CTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTCTGCCGCACTTTCTCC

8401 ValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAlaAlaTrpGluThrAla  
GTCTACTACCTCACCCGTGACCCCTACAACCCCCCTGCGAGAGCTGCGTGAGACAGCA  
CAGATGATGGAGTGGGCACCTGGATGTGGGGGAGCGCTCTCGACGCACCCCTCTGTCGT

8461 ArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPheAlaProThrLeuTrp  
AGACACACTCCAGTCAATTCTGGCTAGGCAACATATCATGTTTGGCCCCACACTGTGG  
TCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAACGGGGGTGTGACACC

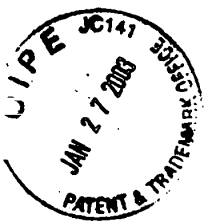


FIG. 72X

AlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAlaArgAspGlnLeuGlu  
8521 GCGAGGATGATAGTATGATGACCCATTCTTTAGCGCTCTATAGCCAGGACGACTTGAA  
CGCTCCTACTATGACTACTGGGTAAGAATAAGCAGGAATATCGGTCCCTGGTCAACTT  
8581 GlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGluProLeuAspLeuPro  
CAGGCCCTCGATTGCGAGATCTACGGGCGCTGCTACTCCATAGAACCACTTGATCTACCT  
GTCCGGGAGCTAACGCTCTAGATGCCCGGACGATGAGGTATCTTGGAAGTATGGA  
8641 ProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHisSerTyrSerProGly  
CCAATCATTCAAAGACTCCCATGGCCCTCAGCGCATTTTCACTCCACAGTTACTCTCCAGGT  
GGTTAGTAAAGTTTCTGAGGTACCGGAGTCCGCTAAAGTGAGGTGTCAATGAGAGGTCCA  
8701 GluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValProProLeuArgAlaTrp  
GAAATTATAGGGTGGCGCGCATGCCCTCAGAAAACTGGGGTACCGCCCTTGCGAGCTTG  
CTTTAATTATCCCAACCGCGGTACGAGTCTTTTGAACCCCATGGCGGGAACGCTCGAACCC  
8761 ArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGlyGlyArgAlaAlaIle  
AGACACCGGGCGCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGAGCGAGGCTGCCATA  
TCTGTGGCCCGGGCGCTCGCAGGCGGATCCGAAGACCGGTCTCCCTCCGACGGTAT  
8821 CysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLysLeuThrProIleAla  
TGTCGCAAGTACCTCTTCAACTGGGCACTAAGAACAAAGCTCAAACTCACTCCAAATAGCG  
ACACCGTTCAATGAGAAAGTTGACCCGTCATTTCTGTTCGAGTTTGAGTGAGGTTATCCG

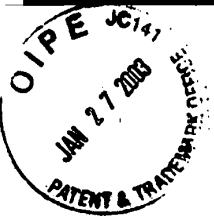


FIG. 72Y

8881  
AlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyrSerGlyGlyAspIle  
GCCGCTGGCCAGCTGACTGTGCCGCTGTTCAACGGCTGCTACAGCGGGGAGACATT  
CGCGACCCGCTCGACCTGAACAGGCCGACCAAGTGCAGCCGATGTGCCCCCTCTGTAA

8941  
TyrHisSerValSerHisAlaArgProArgTyrIleTyrPheCys  
TATCACAGCGTGTCTCATGCCCCCGCCCTGATCTGGTTTGCCC  
ATAGTGTCCACAGAGTACGGGGCGGGGACCTAGACCAAAACGGG



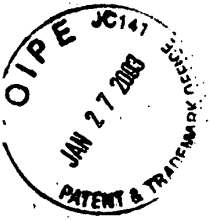


1 GluPheGlySerValIleProThrSerGlyAspValValValAlaThrAspAlaLeu  
GAATTCGGGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTGGCAACCGATGCCCTC  
CTTAAGCCCAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCACCGTTGGCTACGGGAG  
1 ECOR1, 7 NLAIIV, 8 AVA2 SAU96, 15 FOK1, 24 NSPB11, 26 FNU4H  
1, 52 SFAN1, 57 MNL1, 60 NLAI11,  
61 MetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsnThrCysValThrGln  
ATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAATACGTGTGTACCCAG  
TACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTATGCACACAGTGGGTC  
65 HPA11, 74 HPA11, 83 TAQ1, 85 HINF1, 90 HPH, 106 AFL111 MA  
E2, 112 MAE3, 113 HPH,  
121 ThrValAspPheSerLeuAspProThrPheThrIleGluThrIleThrLeuProGlnAsp  
ACAGTCGATTTCAGCCTTGACCCCTACCTTCACCATGAGACAATCACGCTCCCCAAGAT  
TGTCAGCTAAAGTCGGAAGTGGGATGGAAGTGGAAGTCTGTTAGTGCGAGGGGGTTCTA  
125 TAQ1, 149 HPH, 178 SFAN1,  
181 AlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLysProGlyIleTyrArg  
GCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAGCCAGGCATCTACAGA  
CGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTCGGTCCGTAGATGTCT  
198 MAE2, 226 ECOR11 SCRF1, 230 SFAN1,  
241 PheValAlaProGlyGluArgProProAlaCysSerThrArgProSerSerValSerAla  
TTTGTGGCACCGGGGGAGCGCCCTCCGGCATGTTGACTCGTCCGTCCTCTGTGAGTGCC  
AAACACCGTGGCCCCCTCGCGGGAGGCCGTACAAGCTGAGCAGGCAGGAGACACTCACGG  
246 BAN1 NLAIIV, 250 HPA11 NC11 SCRF1, 257 HAE11, 258 HHA1, 2  
62 MNL1, 265 HPA11, 268 NSPC1, 269 NLAI11, 274 TAQ1, 276 HIN  
F1, 287 MNL1, 296 BSP1286,  
301 ArgIle  
CGAATTC  
GCTTAAG  
302 ECOR1,  
361

FIG. 74

FIG. 75

-----Overlap with 6k-----  
1 TyrHisSerValSerHisAlaArgProArgTyrPheCysLeuLeuLeuAla  
TTATCACAGCGTGTCTCATGCCGCGCGCTGGATCTGGTTTGGCTACTCCTGCTGC  
AATAGTGTCCACAGAGTACGGCGCGCGCGACCTAGACCACAAACGGATGAGACGACG  
61 AlaGlyValGlyIleTyrLeuLeuProAsnArgOP  
TGCAGGGGTAGGCATCTACTCTCCCAACCGATGAGGTGGGTAACACTCCGGCC  
ACGTCCCATCCGTAGATGAGAGGGGTTGGCTACTTCCAACCCCATTTGTGAGGCCGG  
121 T  
A



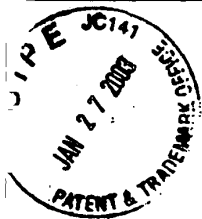
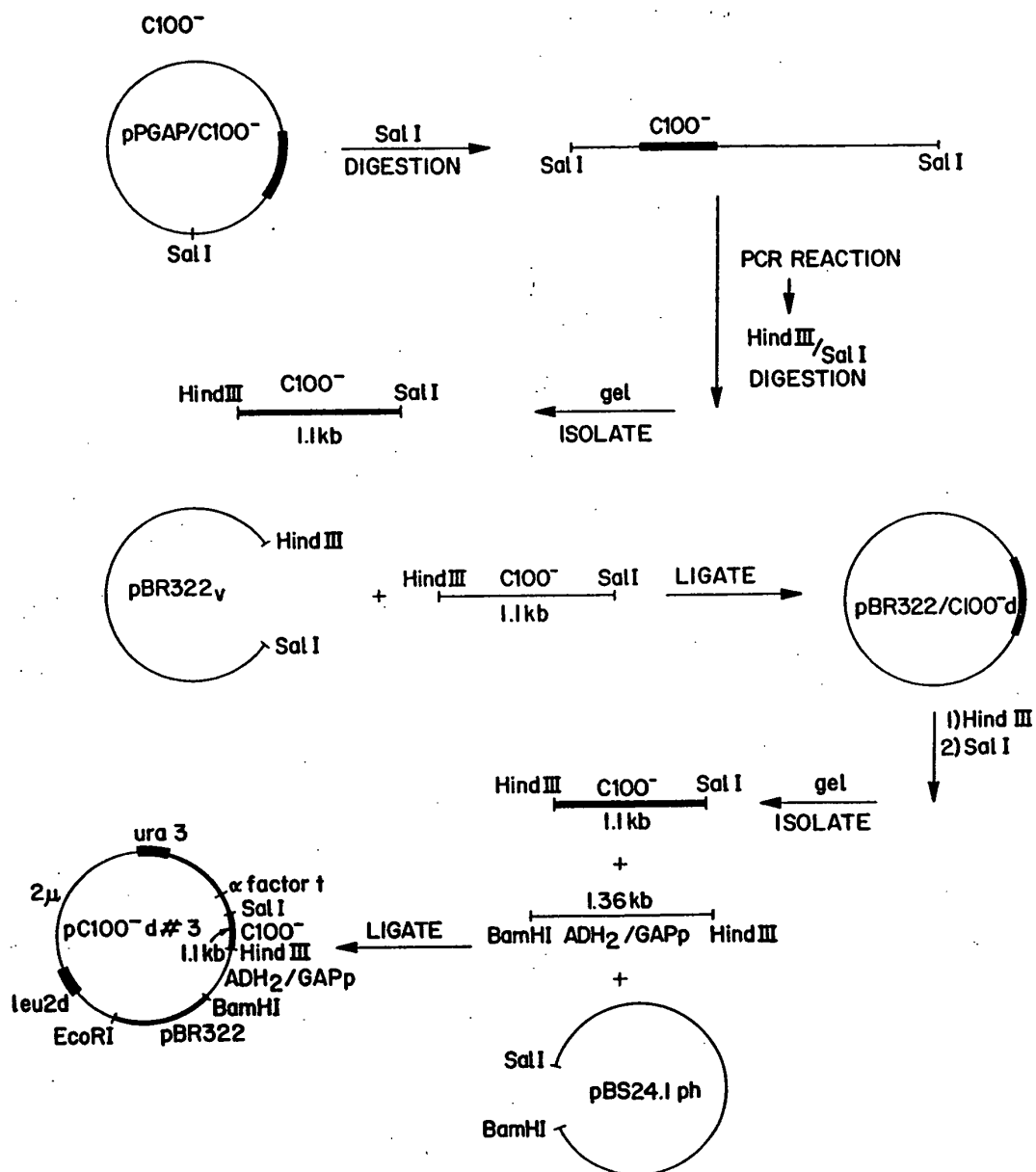


FIG. 76





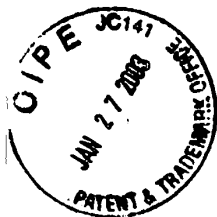
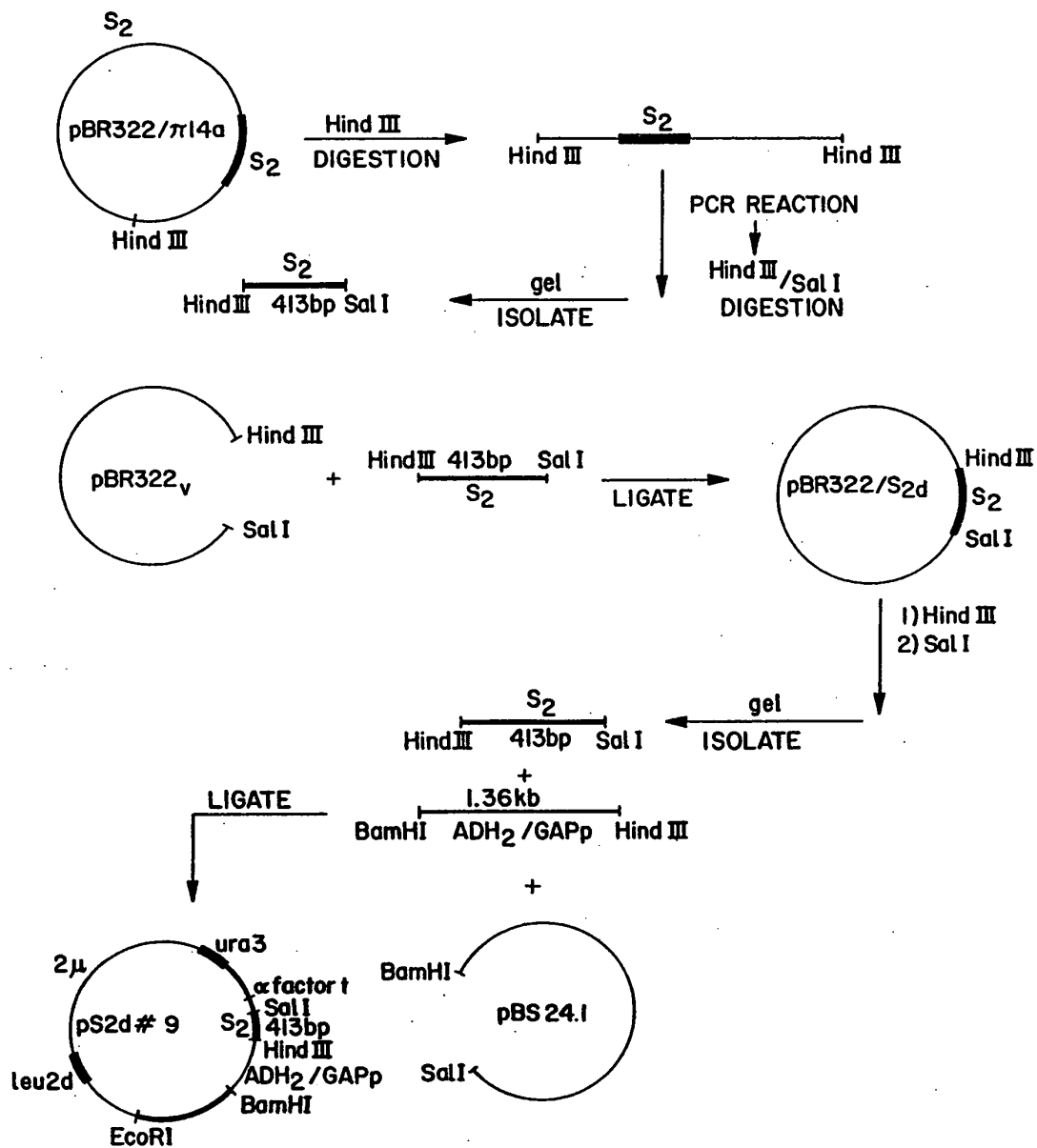


FIG. 77



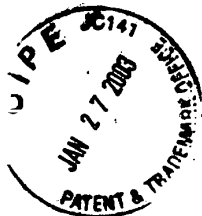
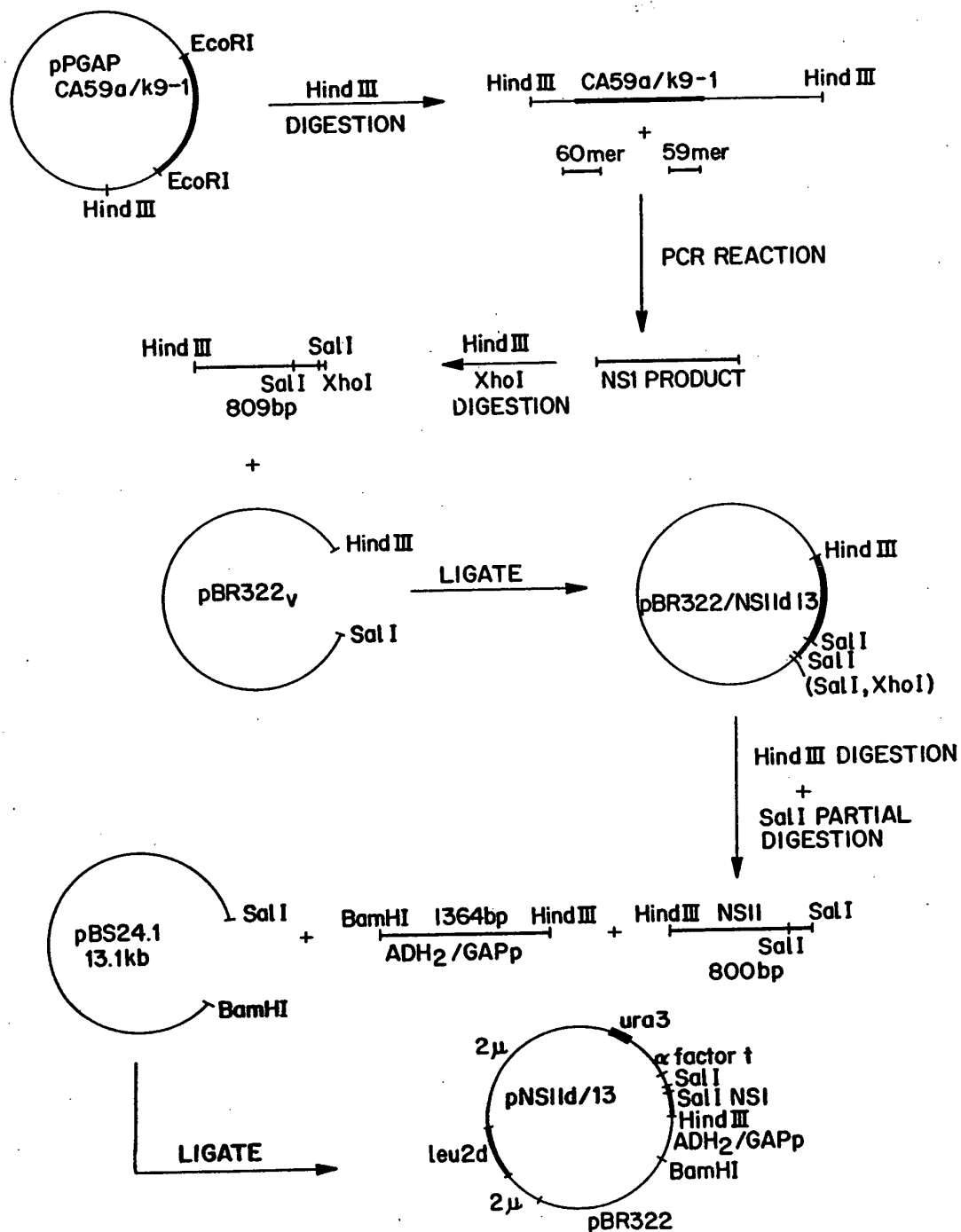


FIG. 78





## FIG. 79A

- 2 AlaValAspPheIleProValGluAsnLeuGluThrThrMetArgSerProValPheThr  
GCGGTGGACTTTATCCCTGTGGAGAACCCTAGAGACAACCATGAGGTCCCCGGTGTTCACG  
CGCCACCTGAAATAGGGACACCTCTTGATCTCTGTTGGTACTCCAGGGGCCACAAGTGC  
29 MAE1, 40 NLA111, 43 MNL1, 45 AVA2 NLA1V SAU96, 49 NC11 SC  
RF1, 50 HPA11,
- 62 AspAsnSerSerProProValValProGlnSerPheGlnValAlaHisLeuHisAlaPro  
GATAACTCCTCTCCACCAGTAGTGCCCCAGAGCTTCCAGGTGGCTCACCTCCATGCTCCC  
CTATTGAGGAGAGGTGGTCATCACGGGGTCTCGAAGGTCCACCGAGTGGAGGTACGAGGG  
69 MNL1, 83 BSP1286, 92 ALU1, 97 ECOR11 SCRF1, 106 HPH, 109  
MNL1, 113 NLA111,
- 122 ThrGlySerGlyLysSerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLysVal  
ACAGGCAGCGGCAAAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATAAGGTG  
TGTCGCTCGCCGTTTTCGTGGTTCCAGGGCCGACGTATACGTTCGAGTCCCGATATTCCAC  
126 BBV FNU4H1, 127 NSPB11, 129 FNU4H1, 145 AVA2 NLA1V SAU96  
, 148 NC11 SCRF1, 149 HPA11, 152 BBV FNU4H1, 156 NDE1, 161 B  
BV FNU4H1, 163 ALU1, 165 DDE1,
- 182 LeuValLeuAsnProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAla  
CTAGTACTCAACCCCTCTGTTGTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCT  
GATCATGAGTTGGGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCGA  
182 MAE1, 184 SCA1, 185 RSA1, 195 MNL1, 203 BBV FNU4H1, 228  
AFL111 NSPC1, 229 NLA111,
- 242 HisGlyIleAspProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIle  
CATGGGATCGATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATC  
GTACCCTAGCTAGGATTGTAGTCTTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAG  
242 NLA111, 246 BIN1, 247 MBO1 SAU3A, 248 CLA1, 249 TAO1, 25  
1 BIN1 MBO1 SAU3A, 264 AVA2 SAU96, 267 HPA11 NC11 SCRF1, 271  
HPH, 291 BBV FNU4H1,
- 302 ThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAsp  
ACGTACTCCACCTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGAC  
TGCATGAGGTGGATGCCGTTCAAGGAACGGCTGCCGCCCCACGAGCCCCCGGAATACTG  
302 MAE2, 304 RSA1, 340 BSP1286 HGIA, 343 AVA1, 350 HAE11, 3  
51 HHA1,
- 362 IleIleIleCysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThr  
ATAATAATTTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACT  
TATTATTAAACACTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGA  
372 MAE3, 391 FOK1, 392 SFAN1, 399 FOK1,
- 422 ValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrPro  
GTCCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTGTGCTCGCCACCGCCACCCCT  
CAGGAAGTGGTTCGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGA  
431 TTHIII2, 435 ALWN1, 461 BSP1286 HGIA, 479 MNL1,



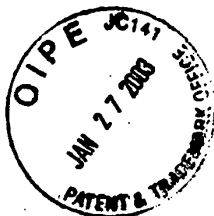
## FIG. 79B

- 482 ProGlySerValThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGly  
CCGGGCTCCGTCACGTGCCCCATCCCAACATCGAGGAGGTGCTCTGTCCACCACCGGA  
GGCCCGAGGCAGTGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCT
- 482 HPA11 NC11 SCRF1, 484 BAN11 BSP1286, 485 NLA1V, 491 MAE3  
, 497 BSP1286, 503 FOK1, 513 TAQ1, 515 MNL1, 518 MNL1, 537 H  
PA11,
- 542 GluIleProPheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeu  
GAGATCCCTTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGAGACATCTC  
CTCTAGGGAAAAATGCCGTTCCGATAGGGGGAGCTTCATTAGTCCCCCTCTGTAGAG
- 543 XHO2, 544 BIN1 MBO1 SAU3A, 571 MNL1, 573 TAQ1,
- 602 IlePheCysHisSerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGly  
ATCTTCTGTCAATCAAAGAAGAGTGCGACGAACTCGCCGCAAAGCTGGTTCGATTGGGC  
TAGAAGACAGTAAGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCG.
- 603 MBO11, 619 MBO11, 638 FNU4H1, 645 ALU1, 660 SFAN1,
- 662 IleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAsp  
ATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGTCCGTCATCCGACCAGCGGCGAT  
TAGTTACGGCACCGGATGATGCGCCAGAAGTGCACAGGCAGTAGGGCTGGTCCGCGCTA
- 672 HAE1, 673 HAE111, 682 NSPB11 SAC2, 683 THA1, 693 AFL111  
MAE2, 703 FOK1, 712 NSPB11, 714 FNU4H1,
- 722 ValValValValAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerVal  
GTTGTCTGTCGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTG  
CAACAGCAGCACCGTTGGCTACGGGAGTACTGGCCGATATGCCGCTGAAGCTGAGCCAC
- 740 SFAN1, 745 MNL1, 748 NLA111, 753 HPA11, 762 HPA11, 771 T  
AQ1, 773 HINF1, 778 HPH,
- 782 IleAspCysAsnThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThr  
ATAGACTGCAATACGTGTGTACCCAGACAGTCGATTTTCAGCCTTGACCTACCTTCACC  
TATCTGACGTTATGCACACAGTGGGTCTGTACGCTAAAGTCGGAAGTGGGATGGAAGTGG
- 794 AFL111 MAE2, 800 MAE3, 801 HPH, 813 TAQ1, 837 HPH,
- 842 IleGluThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThr  
ATTGAGACAATCACGCTCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACT  
TAACTCTGTTAGTGCAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGA
- 866 SFAN1, 886 MAE2,
- 902 GlyArgGlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMet  
GGCAGGGGGAAGCCAGGCATCTACAGATTTGTGGCACCGGGGAGCGCCCTCCGGCATG  
CCGTCCCCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGAGGCCGTAC
- 914 ECOR11 SCRF1, 918 SFAN1, 934 BAN1 NLA1V, 938 HPA11 NC11  
SCRF1, 945 HAE11, 946 HHA1, 948 BGL1, 951 MNL1, 954 HPA11, 9  
57 NSPC1, 958 NLA111,
- 962 PheAspSerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThr  
TTCGACTCGTCCGTCTCTGTGAGTGCTATGACGAGGCTGTGCTTGGTATGAGCTCAGC  
AAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGC
- 963 TAQ1, 965 HINF1, 976 MNL1, 992 HGA1, 1003 TTH112, 1013  
BAN11 BSP1286 HGIA SAC1, 1014 ALU1,



## FIG. 79C

- 1051 RSA1, 1054 NLA111, 1063 AVA1 NCI1 SCRF1 SMA1, 1064 HPA1  
1 NCI1 SCRF1, 1081 ECOR11 SCRF1,
- 1082 GlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHis  
CAGGACCATCTTGAATTTTGGGAGGGCGTCTTACAGGCTCACTCATATAGATGCCAC  
GTCCTGGTAGAACTTAAACCCCTCCCGCAGAAATGTCGGAGTGAGTATATCTACGGGTG
- 1084 AVA2 SAU96, 1103 MNL1, 1106 AHAl1, 1107 HGA1, 1117 HAE1  
STU1, 1118 HAE111, 1120 MNL1, 1133 SFAN1,
- 1142 PheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAla  
TTTCTATCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCC  
AAAGATAGGGTCTGTTTCGTCTCACCCCTCTTGAAGGAATGGACCATCGCATGGTTCGG
- 1183 ECOR11 SCRF1, 1192 RSA1, 1201 DRA3,
- 1202 ThrValCysAlaArgAlaGlnAlaProProSerTrpAspGlnMetTrpLysCysLeu  
ACCGTGTGGCTAGGGCTCAAGCCCTCCCCATCGTGGGACCAGATGTGGAAGTGTGTTG-  
TGGCACACGCGATCCGAGTTCGGGGAGGGGTAGCACCTGGTCTACACCTTCACAAAC
- 1209 HHA1, 1212 MAE1, 1215 BAN11 BSP1286, 1226 MNL1, 1239 NL  
AlV, 1240 AVA2 SAU96, 1256 TTHII12, 1261 HINF1,
- 1262 IleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaVal  
ATTCGCCCTCAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGCGCTGTT  
TAAGCGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAA
- 1267 MNL1, 1279 MNL1, 1282 NCO1, 1283 NLA111, 1286 SAU96, 12  
87 HAE111, 1313 HAE11, 1314 HHA1,
- 1322 GlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAla  
CAGAATGAAATCACCTGACGCACCCAGTCACCAAATACATCATGACATGTCATGTCGGCC  
GCTTACTTTAGTGGGACTGCGTGGGTTCAGTGGTTATGTAGTACTGTACGTACAGCCGG
- 1332 HPH, 1339 HGA1, 1349 MAE3, 1350 HPH, 1363 NLA111, 1367  
NSPC1, 1368 NLA111, 1369 AVA3 NSI1, 1371 NSPC1, 1372 NLA111,  
1377 CFR1 XMA3, 1378 HAE111,
- 1382 AspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAla  
GACCTGGAGGTCGTACAGAGCACCTGGGTGCTCGTTGGCGGCGTCTGGCTGCTTTGGCC  
CTGGACCTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCCGAGGACGACGAAACCGG
- 1384 ECOR11 SCRF1, 1385 GSU1, 1388 MNL1, 1394 MAE3, 1399 BSP  
1286 HGIA, 1404 ECOR11 SCRF1, 1409 BSP1286 HGIA, 1419 FNU4H1  
, 1421 AHAl1, 1422 HGA1, 1426 ECOR11 SCRF1, 1430 BBV FNU4H1,  
1437 CFR1, 1438 HAE111, 1439 FNU4H1, 1441 THAl,
- 1442 AlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeuSerGlyLys  
GCGTATTGCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCGGGGAAG  
CGCATAACGGACAGTTGTCCGACGCACAGTATCACCCGTCCAGCAGAACAGGCCCTTC
- 1453 HINC11, 1461 BBV FNU4H1, 1494 HPA11 NCI1 SCRF1, 1501 NA  
El,
- 1502 ProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCys  
CCGGCAATCATACCTGACAGGGAAGTCTCTACCGAGAGTTCGATGAGATGGAAGAGTGC  
GGCCGTTAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCAGC
- 1502 HPA11, 1528 MNL1, 1542 TAQ1, 1553 MBO11, 1558 BSP1286 H  
GIA,
- 1562 SerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLys  
TCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAG  
AGAGTCGTGAATGGCATGTAGCTCGTTCCTACTACGAGCGGCTCGTCAAGTTCGTCTTC
- 1563 DDE1, 1576 RSA1, 1581 TAQ1, 1590 FOK1, 1594 SFAN1, 1612



## FIG. 79D

- TTHIII2, 1621 HAE111 SAU96,
- 1622 AlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGln  
GCCCTCGGCCTCTGTCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAG  
CGGGAGCCGGAGGACGTCTGGCGCAGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTC
- 1624 MNL1, 1628 HAE111, 1630 MNL1, 1634 PST1, 1639 TTHIII1,  
1642 THA1, 1643 HGA1, 1658 MNL1,
- 1682 ThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGly  
ACCAACTGGCAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACCTTCATCAGTGGG  
TGGTTGACCGTTTTTGTAGCTCTGGAAGACCGCTTCGTATACACCTTGAAGTAGTCACCC
- 1697 AVA1 XHO1, 1698 TAQ1, 1718 NDE1,
- 1742 IleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMet  
ATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCGCCATTGCTTCATTGATG  
TATGTTATGAACCGCCCGAACAGTTGCGACGGACCATTTGGGGCGGTAACGAAGTAACACTAC-
- 1762 HINC11, 1768 BBV FNU4H1, 1772 ECOR11 SCRF1, 1775 BSTE2,  
1776 MAE3,
- 1802 AlaPheThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIle  
GCTTTTACAGCTGCTGTCACCAGCCCACTAACCACTAGCCAAACCCCTCTCTCAACATA  
CGAAAATGTGACGACAGTGGTTCGGGTGATTGGTGATCGGTTGGGAGGAGAAGTTGTAT
- 1809 ALWN1 NSPB11 PVU11, 1810 ALU1, 1811 BBV FNU4H1, 1817 MA  
E3, 1818 HPH, 1836 MAE1, 1846 MNL1, 1849 MNL1, 1851 MBO11,
- 1862 LeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGly  
TTGGGGGGGTGGGTGGCTGCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGC  
AACCCCCCACCACCGACGGGTGCGAGCGCGGGGGCCACGGCGATGACGGAAACACCCG
- 1877 BBV FNU4H1, 1884 ALU1, 1889 FNU4H1, 1895 NC11 SCRF1, 18  
96 HPA11, 1898 BAN1 NLA1V, 1901 FNU4H1, 1919 HAE11, 1920 HHA  
1,
- 1922 AlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIle  
GCTGGCTTAGCTGGCGCCGCCATCGGCAGTGTGGACTGGGGAAGGTCTCTCATAGACATC  
CGACCGAATCGACCGCGGGGTAGCCGTACAACCTGACCCCTTCAGGAGTATCTGTAG
- 1927 DDE1, 1930 ALU1, 1934 AHA11 BAN1 HAE11 NAR1 NLA1V, 1935  
HHA1, 1937 FNU4H1, 1966 AVA2 SAU96, 1969 MNL1, 1978 FOK1,
- 1982 LeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGly  
CTTGACGGGTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGACGGT  
GAACGTCCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCA
- 1995 HHA1, 1996 THA1, 2010 BAN11 BSP1286 HGIA SAC1, 2011 ALU  
1, 2021 BSM1, 2029 MBO1 SAU3A, 2032 NLA111, 2039 HPH,
- 2042 GluValProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAla  
GAGGTCCCTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCTCTCGCCCCGAGCC  
CTCCAGGGGAGGTGCCTCTTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCTCGG
- 2042 MNL1, 2044 AVA2 NLA1V SAU96, 2049 MNL1, 2057 MNL1, 2059  
AVA2 SAU96, 2060 TTHIII1, 2062 ECOR11 SCRF1, 2083 FOK1, 208  
6 MNL1, 2093 NC11 SCRF1, 2094 HPA11, 2096 NLA1V, 2097 BAN11  
BSP1286, 2101 MNL1,
- 2102 LeuValValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGly  
CTCGTAGTCGGCGTGGTCTGTGTCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGG  
GAGCATCAGCCGCACGACACGTCGTTATGACCGCGCGGTGCAACCGGGCCCGCTCCCC
- 2123 BBV FNU4H1, 2134 HHA1, 2136 NAE1, 2137 HPA11, 2142 MAE2  
, 2147 HAE111 SAU96, 2149 AVA1 NC11 SCRF1 SMA1, 2150 HPA11 N



## FIG. 79E

CI1 SCRF1, 2156 MNL1,

2162 AlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSer  
GCAGTGCAGTGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGAACCATGTTTCCCC  
CGTCACGTCACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGG

2172 FOK1, 2179 HPA11, 2196 MNL1, 2199 AVA1 NC11 SCRF1 SMA1,  
2200 HPA11 NC11 SCRF1, 2205 NLA1V, 2210 NLA111,

2222

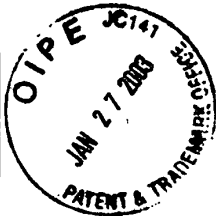


FIG. 80A

Human 23

GlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeuGlyGlyArgAla  
1 GGCTTCGCCGACCTCATGGGTACATACCGTCGTCGGCGCCCTCTTGGAGGCCGTGCC  
ArgAlaLeuAlaHisGlyValArgValLeuGluAspGlyValAsnTyrAlaThrGlyAsn  
61 AGGGCCCTGGCGCACGGCGTCCGGGTTTGGAGACGGCGTGAACATATGCAACAGGGAAC  
CG A  
LeuProGlyCysSerPheSerIlePheLeuLeuAlaLeuLeuSerCysLeuThrValPro  
121 CTTCCCTGGTTGCTCCTTTTCTATCTTCCCTTCTGGCCCTACTCTCTTGCCCTGACCCGTGCC  
GA T  
AlaSerAlaTyrGlnValArgAsnSerThrGlyLeuTyrHisValThrAsnAspCysPro  
181 GCTTCAGCCTACCAAGTGGCAACTCTACGGGGCTTTACCATGTCAACCAATGATTGCCCT  
AsnSerSerIleValTyrGluAlaAlaAspAlaIleLeuHisAlaProGlyCysValPro  
241 AACTCGAGTATTGTACGAGGCGCGCGATGCCATCCTGCACGCTCCGGGGTGTGTCCCT  
T C  
CysValArgGluAspAsnValSerArgCysTrpValAlaValThrProThrValAlaThr  
301 TGCGTTCGCGAGGATAACGTCTCGAGATGTTGGGTGGCGGTGACCCCCACGGTGGCCACC  
G T  
LysAspGlyLysLeuProThrThrGlnLeuArgArgHisIleAspLeuLeuValGlySer  
361 AAGGACGGCAAACTCCCCACAACGACGCTTCGACGTCAATCATCGATCTGCTTGTCTCGGAGC  
C A  
AlaThrLeuCysSerAlaLeuTyrValGlyAspLeuCysGlySerIlePheLeuValGly  
421 GCCACCCCTCTGCTCGGCCCTCTACGTGGGGGACCTTGGGGTCCCATCTTTCTTGTCTGGT  
T  
GlnLeuPheThrPheSerProArgArgHisTrpThrThrGlnAspCysAsnCysSerIle  
481 CAACTGTTTACCTTCTCTCCAGGCGGCCACTGGACGACGACGACTGCAACTGTTCTATC  
C





# FIG. 80B

541 TyrProGlyHisIleThrGlyHisArgMetAlaTrpAspMetMetMetAsnTrpSerPro  
TATCCCGGCCATATAACGGTCAACCGCATGGCATGGATGATGATGAATGATGGTCCCT  
G

601 ThrAlaAlaLeuValAlaGlnLeuLeuArgIleProGlnAlaIleLeuAspMetIle  
ACGGCGGCATTGGTAGTAGCTCAGCTGCTCCGGATCCCAAGCCATCTTGGACATGATC  
G AG

661 AlaGlyAlaHisTrpGlyValLeuAlaGlyMetAlaTyrPheSerMetValGlyAsnTrp  
GCTGGTGCTCACTGGGGAGTCCCTGGCGGCATGGCGTATTCTCTCCATGTTGGGGAACCTGG  
G

721 AlaLysValLeuValLeuLeuLeuPheAlaGlyValAlaAspAlaGluThrHisArgThr  
GCGAAGGTCCTGCTAGTGTGCTTCTATTGCGGGCTCGACGCGGAAACCCACCGTACC  
G

781 GlyGlySerAlaAlaArgSerThrAlaGlyValAlaSerLeuPheThrProGlyAlaArg  
GGGGAAGTGCCTCCCGCAGCACGGCTGGAGTTGCTAGTCTCTTCAACACCGCGCTAGG  
C T A

841 GlnAsnIleGlnLeuIleAsnThrAsnGlySerTrpHisIleAsnSerThrAlaLeuAsn  
CAGAACATCCAGCTGATCAACACCAACGGCAGTTGGCACATCAATAGTACGGCCTTGAAC  
AT

901 CysAsnAspSerLeuThrThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn  
TGCAATGACAGCCTTACCACCGCTGGTTAGCGGGCTTTTCTATCACCATAAATTCAAC  
A

961 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAlaGln  
TCTTCAGGCTGTCCCGAGAGGTTGGCCAGCTGCCGACCCCTCACCGGATTTTGCCCCAGG  
G A

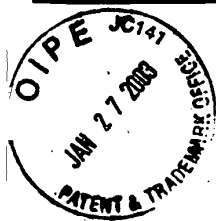


FIG. 81A

Human 27

1 GlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeuGlyGlyAlaAla  
GGCTTCGCCGACCTCATGGGTACATCCGCTCGTCGGCTCCTCTTGGGGCGCTGCC

61 ArgAlaLeuAlaHisGlyValArgValLeuGluAspGlyValAsnTyrAlaThrGlyAsn  
AGGGCCCTGGGCATGGCGTCCGGTTCTGGAAGACGGCGTGAACATATGCAACAGGGAAC

121 LeuProGlyCysSerPheSerIlePheLeuLeuAlaLeuLeuSerCysLeuThrValPro  
CTTCCTGGTTGCTCTTTCTCTATCTTCCTTCTGGCTCTGCTCTCTGACCCGTGCC

181 AlaSerAlaTyrGlnValArgAsnSerSerGlyIleTyrHisValThrAsnAspCysPro  
GCATCGGCCCTACCAAGTAGCGAACTCCTCGGGCATTTACCATGTACCAATGATTGCCCT

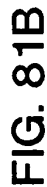
241 AsnSerSerIleValTyrGluThrAlaAspThrIleLeuHisSerProGlyCysValPro  
AATTCGAGTATTGTGTACGAGACGGCCGACACCATCTACACTCTCCGGGTGTGTCCCT  
C

301 CysValArgGluGlyAsnAlaSerLysCysTrpValProValAlaProThrValAlaThr  
TGCGTTCGGAGGGTAACGCCTCGAAATGTTGGGTGCCGGTAGCCCCCACAGTGGCCACC  
G

361 ArgAspGlyAsnLeuProAlaThrGlnLeuArgArgHisIleAspLeuLeuValGlySer  
AGGGACGGCAACCTCCCCGCAACGCAGCTTCGACGTACACATCGATCTGCTTGTCTGGGAGT  
G

421 AlaThrLeuCysSerAlaLeuTyrValGlyAspLeuCysGlySerValPheLeuValGly  
GCCACCCCTTGTCTCGGCCCTCTATGTGGGGACTGTGTGGGTCTGTCTTCTTGTCTCGGT  
C

481 GlnLeuPheThrPheSerProArgArgHisTrpThrThrGlnAspCysAsnCysSerIle  
CAACTGTTCACTTTCTCCCCCAGGGCCACTGGACAACGCAAGATTGCAACTGCTCTATC  
A



961 SerSerGlyCysProGluArgMetAlaSerCysArgProLeuAlaAspPheAspGln  
TCCTCAGGCTGCCCCGAGAGGATGGCCAGCTGTAGGCCCTTGCAGATTTCGACCAGG



FIG. 82A

1. human 27 2. HCV 1 3. human 23

```
1 CGGCTTCGCCGACCTCATGGGGTACATCCGCTCGTCGGCGCTCCTCTTGGGGCGGTGCCAGGGCCCTGGC
  *****
1 CGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCTCTTGGAGGGCGTGCCAGGGCCCTGGC
  *****
1 CGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCTCTTGGAGGGCGTGCCAGGGCCCTGGC
  *****
73 GCATGGCGTCGGGTTCTGGAAGACGGCGTGAACATATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTAT
  *****
73 GCATGGCGTCGGGTTCTGGAAGACGGCGTGAACATATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTAT
  *****
73 GCAGGGCGTCGGGTTTGGGAAGACGGCGTGAACATATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTAT
  *****
145 CTTCCCTTCGGCTCTGCTCTCTTGCCCTGACCGTGCCCCGCaTCGGCCCTACCAAGTaCGAACTCCTCGGGCaT
  *****
145 CTTCCCTTCGGCCCTGCTCTCTTGCTTGACTTGCTGCTCGCCGCTTCGGCCCTACCAAGTGCGCAACTCCACGGGGCT
  *****
145 CTTCCCTTCGGCCCTaCTCTCTTGCCCTGACCGTGCCCGCTTCaGCCTACCAAGTGCGCAACTcACGGGGCT
  *****
217 TTACCAcGTcACCAATGATGCCCTAAcTCGAGTATGTGTACGAGaCGGCCGAcCaCCATCCTaCACTcCTCC
  *****
217 TTACCAcGTcACCAATGATGCCCTAAcTCGAGTATGTGTACGAGCGGCCGATGCCATCCTGCACaCTCC
  *****
217 TTACCAcGTcACCAATGATGCCCTAAcTCGAGTATGTGTACGAGCGGCCGATGCCATCCTGCACgCTCC
  *****
289 GGGGTGtGTCCCTTGCGTTCCGcGAGGGtAACGCCCTCGAaaTGTTGGGTGcCGgTagCCCCcACaGTGGCCAC
  *****
289 GGGGTGcGTCCCTTGCGTTCCGtGAGGGcAACGCCCTCGAGgTGTTGGGTGGCGaTGACCCCTACGGTGGCCAC
  *****
289 GGGGTGtGTCCCTTGCGTTCCGcGAGGatAAGGtCTCGAGaTGTTGGGTGGCGgTGACCCcACGGTGGCCAC
  *****
```

**FIG. 82B**

```

361 CAGGACGGCAACCTCCCGGCAACGACCTTCGACGTACATCGATCTGCTTCGGGAGtGCCACCTtTG
    *****
361 CAGGAtGGCAACTCCCGCGAGCGACCTTCGACGTACATCGATCTGCTTCGGGAGCGCCACCTCTG
    *** *****
361 CAAGACGGCAACTCCCGCAACGACGCTTCGACGTACATCGATCTGCTTCGGGAGCGCCACCTCTG
    *****

433 CTCGGCCCTCTAtGTGGGGACtTGTCCGGTCTTCTTGTGCGtCAACTGTTCAtTTCTCtCCCGAG
    *****
433 tTCGGCCCTCTACGTGGGGACCTGTGCGGTCTGTCTTCTTGTGCGcCAACTGTTCACCTTCTCtCCAG
    *****
433 CTCGGCCCTCTACGTGGGGACCTtTGC GGTCaTCTTCTTGTGCGtCAACTGTtTtACCtTCTCtCCAG
    *****
505 GCGCCACTGGACAACGCAAGAtTGCACtGTCTATCTACcCCCGCATATACGGGACACCGCATGGCATG
    *****
505 GCGCCACTGGACGACGCAAGgtTGCAtTGTCTATCTATCCCGGCATATAcGGGTCAcCGCATGGCATG
    *****
505 GCGCCACTGGACGACGCAggaCTGCACtGtTCTATCTATCCCGGCATATAcGGGTCAcCGCATGGCATG
    *****
577 GGATATGATGATGAACtGTCCCTACagCAGCGtGTAAAGGCTCAAGCTGTCAgATCCGCAAGCCAT
    *****
577 GGATATGATGATGAACtGTCCCTACGaCGGCGTGTAAAGGCTCAAGCTGTCCGATCCCAcCAAGCCAT
    *****
577 GGATATGATGATGAACtGTCCCTACGgCGGCAtTGTAGtAGCTCAAGCTGTCCGATCCCAcCAAGCCAT
    *****
649 CTTGGACATGATCGCTGTGTCTCACTGGGAGTCTAGCGGGCATAGCGTATTCTCCATGtTGGGAACTG
    *****
649 CTTGGACATGATCGCTGTGTCTCACTGGGAGTCTAGCGGGCATAGCGTATTCTCCATGtTGGGAACTG
    *****
649 CTTGGACATGATCGCTGTGTCTCACTGGGAGTCTAGCGGGCATAGCGTATTCTCCATGtTGGGAACTG
    *****
721 GCGGAAGTCTCTGtGTGTGCTgtTGTCCGCGCTGAtGCGaCAACtLataCCACCGGGGgAATGC
    *****
721 GCGGAAGTCTCTGtGTGTGCTGTGCTATTGcCGGCGTCAcGGAAACCCACgttCACCGGGGgAATGC
    *****
721 GCGGAAGTCTCTGtGTGTGCTgtTGTCCGCGCTCAcGGAAACCCACgttACCGGGGgAATGC
    *****

```



793 tGcCaggaCCaacGcagGcgCTcaaccAGtTtTtagccCAAGCGCCCAAGCAGgAtaTCCAGCTGATCAACAC  
\* \* \* \* \*  
793 CGgCCaCAcTgtGtCTGgAtTgTtagcCTcTcTgCAcCAAGCGCCCAAGCAGaCgTCCAGCTGATCAACAC  
\* \* \* \* \*  
793 CGcCCgCAgcaacGgCTGgAGTgCTAGtCTcTtCAcCAAGCGcCTAgGCAgAcaTCCAGCTGATCAACAC

865 CAACGGCAGTTGGCAcATCAATcGCAcGGcCTtGAACtGtAATGcgAGcCTcGACAcTgGCTGgTAgCgGg  
\* \* \* \* \*  
865 CAACGGCAGTTGGCAcCTCAATAGCAcGGcCTGAACtGCAATGAtAGcCTCAACACcCGGCTGgTgCagG  
\* \* \* \* \*  
865 CAACGGCAGTTGGCAcATCAATAGtACGGcCTtGAACtGCAATGAcAGcCTtAcCAcCGGCTGgTAgCgGg

937 GCTcTTCTATtACCACAaTTCAACTCTTCAGGcTGcCCcGAGAGgATgGCCAGCTgtagCCcCTTgCCGA  
\* \* \* \* \*  
937 GCTTTCTATCAcCAcAGTTCAACTCTTCAGGcTGtCctGAGAGgctAgCCAGCTGCCGACCCCTTACCGA  
\* \* \* \* \*  
937 GCTTTCTATCAcCAtAAATTCAACTCTTCAGGcTGtCCcGAGAGgTtGgCCAAGCTGCCGACCCCTcACCGA

1009 TTtCGACcCAGG  
\* \* \* \* \*  
1009 TTTTGACcCAGG  
\* \* \* \* \*  
1009 TTTTGcCCAGG

FIG. 82C

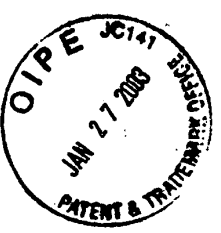


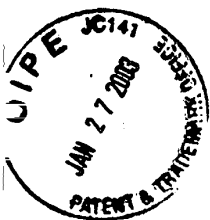
FIG. 83

```

1 GFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNATGNLPCCSFSIFLLALLSCLTPASAYQVRNSGI
*****
1 GFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNATGNLPCCSFSIFLLALLSCLTPASAYQVRNSTGL
*****
1 GFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNATGNLPCCSFSIFLLALLSCLTPASAYQVRNSTGL
*****
73 YHVTNDCPNSSIVYEADTILHSPGCVPCVREGNASKCWVPVAPTVAITRDGILPATQLRRHIDLVSATLC
*****
73 YHVTNDCPNSSIVYEADAILHLPGCVPVREGNASRCWVAMPTVATRDGILPATQLRRHIDLVSATLC
*****
73 YHVTNDCPNSSIVYEADAILHAPGCVPCVREDNVSRCWVAVPTVATKDGLPTQLRRHIDLVSATLC
*****
145 SALYVGDLGCVFLVGOLFETSPRRHWTQDNCNSIYPGHITGHMAWDMMNWSPALVMAQLLRIPQAI
*****
145 SALYVGDLGCVFLVGOLFETSPRRHWTQDNCNSIYPGHITGHMAWDMMNWSPALVMAQLLRIPQAI
*****
145 SALYVGDLGCVFLVGOLFETSPRRHWTQDNCNSIYPGHITGHMAWDMMNWSPALVMAQLLRIPQAI
*****
217 LDMIAGAHWGVLAGIAYFSMVGNWAKVLVLLIFAGVDATtYtTGnAaRTtqaltSffsPGAKOdIQLINT
*****
217 LDMIAGAHWGVLAGIAYFSMVGNWAKVLVLLIFAGVDAETHVtGGSaghtvsgfvSllaPGAKONvQLINT
*****
217 LDMIAGAHWGVLAGIAYFSMVGNWAKVLVLLIFAGVDAETHITGGSaAarstaGvaSLftPGaTONiQLINT
*****
289 NGSWHINRTALNCNaSLdTGwAGlfYyHKFNSSGCCPERMaSCRPIAdFDQ
*****
289 NGSWHINRTALNCNDSLnTGwLAGlfYyHKFNSSGCCPERLaSCRPIlTDfDQ
*****
289 NGSWHINRTALNCNDSLtTGwLAGlfYyHKFNSSGCCPERLaSCRPIlTDfDQ
*****

```

1. human 27
2. HCV 1
3. human 23



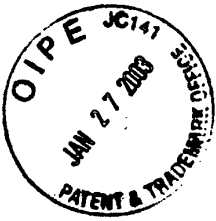


FIG. 84

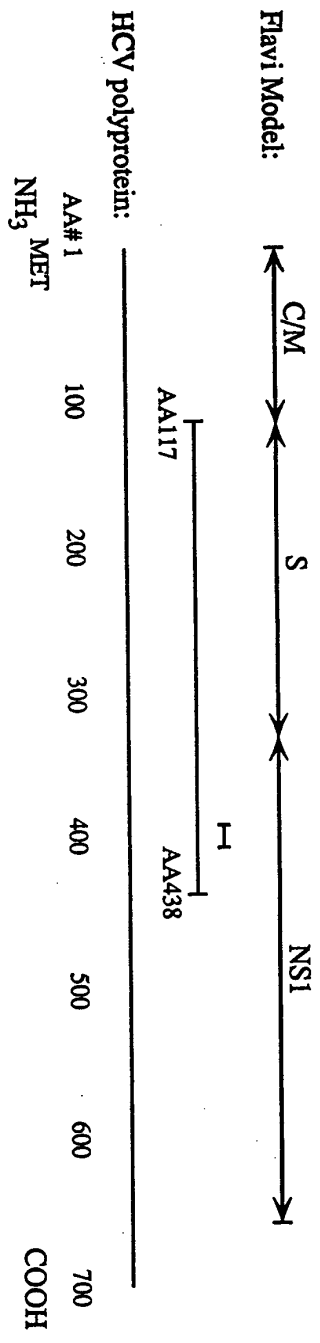




FIG. 85A

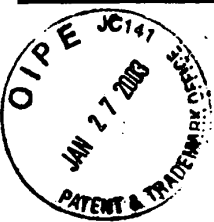
1. ssthorn#8.r (1-587)
2. sSEC1#2.r (1-587)
3. sSHCT18#7.r (1-587)
4. env1.hcv (1-1657)

GA  
||  
GA  
||  
GA

1.  
289 gggtggcgagatgctcctgtctccccgtgctctcgccctagctggggccaccagacccccgycgtag

3 ATTCGCAATTGGGTAAGGTCAATCGATAACCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTC  
3 ATTCGCAATTGGGTAAGGTCAATCGATAACCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTC  
3 ATTCGCAATTGGGTAAGGTCAATCGATAACCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTC  
361 tcgCGCAATTGGGTAAGGTCAATCGATAACCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTC

75 GTCGGCGCCCTCTTGGggggCGCTGCCAGGGCCCTGCGGCATGCGCGTCCGGGTTCTGGAAGACGGCGTGAAC  
75 GTCGGCGCCCTCTTGGAGGCGCTGCCAGGGCCCTGCGGCATGCGCGTCCGGGTTCTGGAAGACGGCGTGAAC  
75 GTCGGCGCCCTCTTGGAGGCGCTGCCAGGGCCCTGCGGCATGCGCGTCCGGGTTCTGGAAGACGGCGTGAAC  
433 GTCGGCGCCCTCTTGGAGGCGCTGCCAGGGCCCTGCGGCATGCGCGTCCGGGTTCTGGAAGACGGCGTGAAC



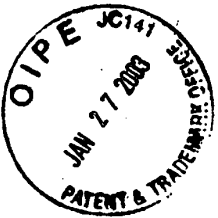
147 TATGCAACAGGGAACCTTCCTGCTGCTGCTCTTCTcTcTCTTCCCTCTGAGCCcTgCTCTCTTgtcTGACcGTG  
147 TATGCAACAGGGAACCTTCCTGCTGCTGCTCTTCTcTATATCTTCCCTCTGAGCCcTgCTCTCTTgtcTGACtGTG  
147 TATGc CAGGGAACCTTCCTGCTGCTGCTCTTCTcTATATCTTCCCTCTGAGCCcTgCTCTCTTgtcTGACtGTG  
505 TATGCAACAGGGAACCTTCCTGCTGCTGCTCTTCTcTATATCTTCCCTCTGAGCCcTgCTCTCTTgtcTGACtGTG  
219 CCGCGTTcAGcCTTACCAAGTgCGCAACTCcAcGGGGcTTTACCAtGTCAcCAAcGATTTGCCcCAACTGcAGt  
219 CCGCGTTcAGcCTTACCAAGTgCGCAACTCcCcGGGGcTTTACCAtGTCAcCAATGATTTGCCcTAACTGcAGc  
219 CCGCGTTcAGcCCcACCAAGTgCGCAACTCCAcGGGGcTTTACCAtGTCAcCAATGATTTGCCcCAACTGcAGT  
577 CCGCGTTcGcCCtAcCCAAGTgCGCAACTCCAcGGGGcTTTACCAtGTCAcCAATGATTTGCCcTAACTGcAGT  
291 ATTGTGTAcGAGGcGCGCGATGcTATCCGTGcAcGcTCCGGGcGTGTCCCTTgCGTTcGcGAGGcTAAGcCC  
291 ATTGTGTAcGAGGcGCGCGATGcCATCCGTGcAcACTCCGGGcGTGTCCCTTgCGTTcAcGAGGcCAAcGTc  
291 ATTGTATAcGAAGcGCGCGAcCGCATCCGTGcAcACTCCGGGcGTGTCCCTTgCGTTcAcGAGGcCAAcGTc  
649 ATTGTGTAcGAGcGCGCGcCGATGcCATCCGTGcAcACTCCGGGcGTcGTCCCTTgCGTTcgtGAGGcCAAcGcc  
363 TCGAGcGTGTGGGTGcCGATGAcCCcCAcGcGTGcCGcCAcGGAcGcGcAGAcTCCcCACAACGcAGcTgCGAc  
363 TCGAGcGTGTGGGTGcCGATGAcCCcCAcGcGTGcCGcCAcGGAcGcGcAGAcTCCcCACAACGcAGcTTGGA  
363 TCGAGcGTGTGGGTGcCGgTGAcCCcCAcGcGTGcCGcCAcGGAcGcGcAGAcTCCcCACAACGcAGcTTGGA  
721 TCGAGcGTGTGGGTGcCGATGAcCCcTAcGcGTGcCGcCAcGGAcGcGcAGAcTCCcCACAACGcAGcTTGGA

435 CGTCACATCGATCTGCTTGTCCGGAGCGCCACCCTCTGCTCGGCCCTCTACGTGGGGGACCTGTGCGGGTCC  
435 CGTCACATCGATCTGCTTGTCCGGAGCGCtACCCTCTGCTCGGCCCTCTACGTGGGGGACCTGTGCGGGTCT  
435 CGTCACATCGATCTGCTTGTCCGGAGCGCCACCCTCTGCTCGGCCCTCTAtGTGGGGGACtTGTGCGGGTCT  
793 CGTCACATCGATCTGCTTGTCCGGAGCGCCACCCTCTGtTCCGCCCTCTACGTGGGGGACcTAtTCCGGGCTCT

507 ATCTTtCTTGTCCGTCACACTGTTcACCCTTCTCTCCAGCGGCCCACTGGACGACGCAAGGTTGCAATTGCTCT  
507 GTCTTcCTTGTCCGTCACACTGTTTACCCTTCTCTCCAGCGGCCCACTGGACGACGCAAGGTTGCAATTGCTCT  
507 GTCTTtCTTGTCCGTCACACTGTTTACCCTTCTCTCCAGCGGCCCACTGGACGACGCAAGGTTGCAATTGCTCT  
865 GTCTTtCTTGTCCGTCACACTGTTcACCCTTCTCTCCAGCGGCCCACTGGACGACGCAAGGTTGCAATTGCTCT

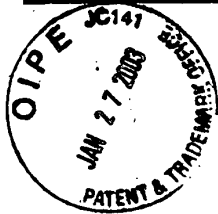
579 ATCGAATTTC  
579 ATCGAATTTC  
579 ATCGAATTTC  
937 ATCtAtccC

FIG. 85C



[illegible]

FIG. 86



AA #117-308 (putative envelope region)

FIG. 87

- |                       |                    |
|-----------------------|--------------------|
| 1) HCT #18 (USA)      | 3 clones sequenced |
| 2) JH23 (USA)         | ?                  |
| 3) JH 27 (USA)        | ?                  |
| 4) PBL-Th (USA)       | 2 clones sequenced |
| 5) EC1 (Italy)        | 3 clones sequenced |
| 6) HCV-1 (chimpanzee) | multiple           |

C/M ← T → S

- 1) (P)  
 2)  
 3)  
 4)  
 5)

6) RNLGKVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNL

- 1) H  
 2)  
 3) S T T  
 4) L  
 5) (F) S

6) PGCSFSIFLLALLSCLTVPASAYQVRNSTGLYHVTNDCPNSSIVYEAADAILH

- 1) Y (H) V V T  
 2) A D V V K T  
 3) S PVA N  
 4) A A R T  
 5) H V T

6) TPGCVPCVREGNASRCWVAMTPTVATRDGKLPATQLRRHIDLLVGSATLCS

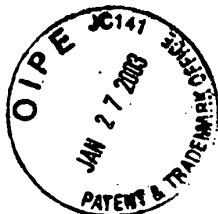
- 1)  
 2) I D  
 3) D  
 4)  
 5) I

6) ALYVGDLGSGVFLVGQLFTFSPRRHWTTQGCNCSI

SUMMARY: "S" AA117-308 (93%)

HCT#18, PBL-Th, EC1(Italy) have 97% homology with HCV-1

JH23 and JH 27 have 96% and 95% homology with HCV-1, respectively



AA#300-438 ( C-terminal region of the putative envelope region and amino ~1/3 of NSI)

- 1) JH23
- 2) JH27
- 3) Japanese isolate (T. Miyamura)
- 4) EC10 (Italy)

?

?

?

2 clones sequenced  
(one nt difference, which did not  
result in an amino acid change)  
multiple

- 5) HCV-1 (chimpanzee)

S ← NSI

A V

A

V S

VM V

- 1) D

- 2) D

- 3)

- 4)

5) TTQGCNCSIYPGHITGHRMAWDMMMNSPTTALVMAQLLRIPQAILDMIAGA

- 1) M

R

ARSTA VA

- 2)

T YT

N AR TQALT F

- 3) L Y

I M

GH R

VQ VT TLT

- 4)

A

I AK TASLTA

5) HWGVLAGIAYFSMVGNWAKVLVLLLFAGVDAETHVTGGSAGHTVSGFVSL

- 1) FS

R I

I

T V

- 2) FT

DI

I R

A D

- 3) FR

S KI V

I R

Q F

- 4) FNL

I

I R

N

5) LAPGAKQNVQLINTNGSWHLNSTALNCNDSLNTGWL

SUMMARY: NS 1 AA 330-660

"Isolate"	%Homology (AA330-438)	%Homology (AA383-405)
JH23	83	57
JH27	80	39
Japanese	73	48
EC10 (Italy)	84	48

FIG. 88

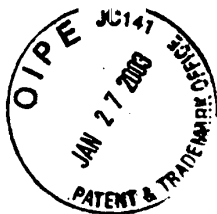


FIG. 89A

5' terminus-----  
CACTCCACCATGAATCACTCCCCTGTGAGGAAGTACTGTCTTCACGCAGAAAGCGTCTAG  
CCATGGCGTTAGTATGAGTGTGCGTGCAGCCTCCAGGACCCCCCTCCCGGGAGAGCCATA  
GTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCTTTCTTGGA  
TCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCGCAAGACTGCTAGCCGAGTAGT  
GTTGGGTGCGGAAAGGCTTGTGGTACTGCCTGATAGGGTGTTCGAGTGCCCCGGGAG-300

(Putative initiator methionine codon)

GTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACCTCAAAAAAACAACGTAA  
CACC AACCGTCGCCACAGGACGTCAAGTTCCCGGGTGGCGGTCAAGTCGTTGGTGGAGT  
TTACTTGTGGCGCGAGGGGCCCTAGATTGGGTGTGCGCGGACGAGAAAGACTTCCGA  
GCGGTGCGAACCTCGAGGTAGACGTACGCTATCCCCAAGGCTCGTCGGCCCGAGGGCAG  
GACCTGGGCTCAGCCCGGGTACCTTGGCCCTCTATGGCAATGAGGGCTGCGGGTGGGC-600  
GGGATGGCTCCTGTCTCCCGTGGCTCTCGGCCTAGCTGGGGCCCCACAGACCCCGGCG  
TAGGTGCGCAATTTGGGTAAGGTATCGATACCTTACGTGCGGCTTCCGCGACCTCAT  
GGGTACATACCGCTCGTCGGCGCCCTCTTGGAGGCGCTGCCAGGGCCCTGGCGCATGG  
CGTCCGGGTTCTGGAAGACGGCGTGAACATGCAACAGGGAACCTTCTGTTGCTCTTT

CTCTATCTTCCTTCTGGCCCTGCTCTTGTGCTTACTGTGCCGCTTCGGCCTACCAAGT-900  
GCGCAACTCCACGGGGCTTTACCACGTACCAATGATTGCCCTAACTCGAGTATTGTGTA  
CGAGGCGGCGGATGCCATCTGCACACTCCGGGGTGCCTCCCTTGCCTTCGTGAGGGCAA  
CGCTCGAGGTGTTGGGTGGCGATGACCCCTACGGTGGCCACAGGGATGGCAAACTCCC  
CGCGACGCGAGCTTCGACGTACATCGATCTGCTTGTGCGGAGCGCCACCTCTGTTCCGC  
CCTCTACGTGGGGGACCTATGCGGGTCTGTCTTTCTTGTGCGGCAACTGTTACCTTCTC-1200  
TCCAGGCGCCACTGGACGACGCAAGGTTGCAATTGCTCTATCTATCCCGGCCATATAAC

GGGTCACCGCATGGCATGGGATATGATGATGAACTGGTCCCTACGACGGCGTTGGTAAT  
GGCTCAGCTGCTCCGGATCCCAAGCCATCTTGGACATGATCGCTGGTGTCTACTGGGG  
AGTCTTGGCGGGCATAGCGTATTTCTCCATGGTGGGGAACCTGGGCGAAGGTCCTGGTAGT  
GCTGCTGCTATTTGCCGGCGTGCAGCGGAAACCCACGTACCGGGGGGAAGTGCCGGCCA-1500  
CACTGTGTCTGGATTTGTTAGCCTCCTCGACACGAGCGCCAAGCAGAACGTCCAGCTGAT  
CAACACCAACGGCAGTTGGCACCTCAATAGCACGGCCCTGAAGTGAATGATAGCCTCAA  
CACC GGCTGGTTGGCAGGGCTTTCTATCACCACAAGTTCAACTCTTCAGGCTGTCTGA  
GAGGCTAGCGAGCTGCCGACCCCTTACCGATTTTGACAGGGCTGGGGCCCTATCAGTTA  
TGCCAACGGAAGCGGGCCCGACGAGCGCCCTACTGCTGGCACTACCCCCAAAACCTTG-1800  
CGGTATTGTGCCCGCGAAGAGTGTGTGTGGTCCGGTATATTGCTTCACTCCAGCCCCGT  
GGTGGTGGGAACGACGAGGTGCGGCGCGCCACCTACAGCTGGGGTGAAAATGATAC  
GGACGTCTTCGTCCTTAACAATACGAGGCCACCGCTGGGCAATTGGTTGCGTTGTACCTG  
GATGAACTCAACTGGATTACCAAAAGTGTGCGGAGCGCCTCCTTGTGTATCGGAGGGGC  
GGGCAACAACACCCTGCACTGCCCCACTGATTGCTTCGCAAGCATCCGGACGCCACATA-2100

CTCTCGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTGCCTGGTCGACTACCCGTATAG  
GCTTTGGCATTATCCTTGTACCATCAACTACCATATTTAAAAATCAGGATGTACGTGGG  
AGGGGTGCAACACAGGCTGGAAGCTGCCTGCAACTGGACGCGGGGCGAACGTTGCGATCT  
GGAAGACAGGGACAGGTCCGAGCTCAGCCGTTACTGCTGACCACTACACAGTGGCAGGT  
CTCCCGTGTTCCTTCAACCCCTACCAAGCTTGTCCACCGGCCTCATCCACCTCCACCA-2400  
GAACATTGTGGACGTGCACTTGTACGGGGTGGGGTCAAGCATCGCGTCTGGGCCAT  
TAAGTGGGAGTACGTCTTCTCTGTTCTTCTGCTTGCAGACGCGCGCTGCTGCTCTG  
CTTGTGGATGATGCTACTCATATCCCAAGCGGAGGCGGCTTGGAGAACCTCGTAATACT  
TAATGCAGATCCCTGGCGGGACGACGCTTGTATCCTTCTCTGTTCTTCTGCTT  
TGCATGGTATTTGAAGGGTAAGTGGGTGCCCGGAGCGGTCTACACCTTCTACGGGATGTG-2700  
GCCTCTCCTCTGCTCCTGTTGGCGTTGCCCGAGCGGGCGTACGCGCTGGACACGGAGGT  
GGCCGCGTCTGTGGCGGTGTTGTTCTGCTGCGGTTGATGGCGCTGACTCTGTACCCATA  
TTACAAGCGCTATATCAGCTGGTGTGTTGGTGGCTTCAATTTTCTGAGAGTGGGA  
AGCGCAACTGCACGTGTGGATTCCCCCCTCAACGTCCGAGGGGGGCGGACGCCGTCAT



FIG. 89B

CTTACTCATGTGTGCTGTACACCCGACTCTGGTATTTGACATCACCAAATTGCTGCTGGC-3000  
CGTCTTCGGACCCCTTTGGATTCTTCAAGCCAGTTTGTCTAAAGTACCTACTTTGTGCG  
CGTCCAAGGCCTTCTCCGGTTCTGCGCTTAGCGCGGAAGATGATCGGAGGCCATTACGT  
GCAAATGGTCATCATTAAGTTAGGGGCGCTTACTGGCACCTATGTTTATAACCATCTCAC  
TCCTCTTCGGGACTGGGCGCACAAAGGCTTGCAGATCTGGCCGTGGCTGTAGAGCCAGT  
CGTCTTCTCCCAAATGGAGACCAAGCTCATACGTGGGGGGCAGATACCGCCGCGTGC GG-3300  
TGACATCATCAACGGCTTGCCTGTTTCCGCCCGCAGGGGCGGGAGATACTGCTCGGGCC  
AGCCGATGGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCATCACGGCGTACGCCCA  
GCAGACAAGGGGCTCCTAGGGTGCATAATCACCAGCCTAACTGGCCGGGACAAAAACCA  
AGTGGAGGGTGAGGTCCAGATTGTGTCAACTGCTGCCCAAACCTTCTGGCAACGTGCAT  
CAATGGGGTGTGCTGGACTGTCTACCACGGGGCGGAACGAGGACCATCGCGTCAACCAA-3600

GGGTCTGTATCCAGATGTATACCAATGTAGACCAAGACCTTGTGGGCTGGCCGCTCC<sup>T</sup>

GCAAGGTAGCCGCTCATTGACACCCTGCACTTGGGGCTCCTCGGACCTTTACCTGGTCA<sup>C</sup>  
GAGGCACGCCGATGTCATTCCCGTGCGCCGGCGGGGTGATAGCAGGGGCAGCCTGCTGTC  
GCCCCGGCCATTTCTACTTGAAGGCTCCTCGGGGGTCCGCTGTTGTGCCCGCGGG  
GCACGCCGTGGGCATTTAGGGCGCGGTTGTCACCCGTGGAGTGGCTAAGCGGTGGA-3900  
CTTTATCCCTGTGGAGAACCTAGAGACAACCATGAGTCCCGGTGTTACCGGATAACTC  
CTCTCCACAGTAGTCCCCAGAGCTTCCAGGTGGCTCACCTCCATGCTCCACAGGCAG  
CGGCAAAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACT  
CAACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGTACATGTCCAAGGCTCATGGGAT

CGATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTC-4200<sup>T</sup>  
CACCTACGGCAAGTTCCTTGCCGACGGCGGGTGTCTGGGGGGCGCTTATGACATAATAAT  
TTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCGGCACGTGCTTGA  
CCAAGCAGAGACTGCGGGGGCGAGACTGTTGTGCTCGCCACCGCCACCCCTCCGGGCTC  
CGTCACTGTGCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCC  
TTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGAGACATCTCATCTTCTG-4500  
TCATTCAAAGAAGAAGTGCAGCAACTCGCCGCAAGCTGGTTCGATTGGGCATCAATGC  
CGTGGCCTACTACCGGGTCTTGACGTGTCCGTATCCCGACCAAGCGGCGATGTTGTCGT

CGTGGCAACCGATGCCCTCATGACCGGCTATACCGCGACTTCGACTCGGTGATAGACTG<sup>A</sup>  
CAATACGTGTGTACCCAGACAGTCGATTTAGCCTTGACCCTACCTTCACCATGAGAC  
AATCAGCTCCCCAGGATGCTGTCTCCGCACTCAACGTGCGGGCAGGACTGGCAGGGG-4800  
GAAGCCAGGCATCTACAGATTTGTGGCACCAGGGGAGCGCCCTCCGGCATGTTGACTC  
GTCCGTCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCGCA  
GACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCGTTGTGCCAGGACCA  
TCTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCATTTCTATC  
CCAGCAAAAGCAGAGTGGGGAGAACCTTCTTACCTGGTAGCGTACCAAGCCACCGTGTG-5100  
CGCTAGGGCTCAAGCCCTCCCCATCGTGGGACAGATGTGGAAGTGTGATTGCGCT  
CAAGCCACCCCTCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAAATGA  
AATCACCCTGACGCACCAAGTCAACAAATACATCATGACATGCATGTCGGCCGACCTGGA  
GGTCGTACGAGCACCTGGGTGCTCGTTGGCGGGCTCCTGGCTGCTTTGGCGCGTATTG  
CCTGTCAACAGGCTGCGTGGTATAGTGGGCAAGGTCGTCTTGTCCGGGAAGCGGCAAT-5400  
CATACCTGACAGGGAAGTCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCA  
CTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGG  
CCTCCTGCAGACCGCTCCCGTCAGGCAGAGGTTATCGCCCTGCTGTCCAGACCAACTG  
GCAAAAACCTCGAGACCTTCTGGGCGAAGCATATGTGGAACCTCATAGTGGGATACAATA  
CTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTAC-5700  
AGCTGCTGTACACAGCCCACTAACCAATAGCCAAACCTCCTCTTCAACATATTGGGGGG  
GTGGGTGGTGGCCAGCTCGCCGCCCGGTGCGCTACTGCTTTTGTGGGCGCTGGCTT  
AGCTGGCGCGCCATCGGCAGTGTGGACTGGGGAAAGGTCTCATAGACATCCTTGCAGG  
GTATGGCGCGGGCTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCC  
CTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCTCTCGCCCGGAGCCCTCGTAGT-6000  
CGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCGGGCGAGGGGGCAGTGCA  
GTGGATGAACCGGTGATAGCCTTCGCTCCCGGGGGAACCATGTTTCCCCACGCACTA  
CGTGGCGGAGAGCGATGCAGCTGCCCGCTCACTGCCATACTCAGCAGCCTCACTGTAAC  
CCAGCTCCTGAGGCGACTGCACCAAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGG



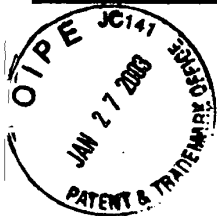


FIG. 89C

TTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTG-6300  
GCTAAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCTGCCAGCGCGG  
GTATAAGGGGGTCTGGCGAGTGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGA  
GATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAA  
CATGTGGAGTGGGACCTTCCCCATTAAATGCCTACACCACGGGCCCCCTGTACCCCCCTTCC  
TGCGCCGAACACTACACGTTGCGCTATGGAGGGTGTCTGCAGAGGAATATGTGGAGATAAG-6600  
GCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTCAAATGCCCGTG  
CCAGGTCCCCTCGCCGAATTTTCACAGAATTGGACGGGGTGCCTACATAGGTTTGC  
GCCCCCTGCAAGCCCTTGTCTGCGGAGGAGGTATCATTAGAGTAGGACTCCACGAATA  
CCCCGTAGGGTCGCAATTACCTTGCAGCCGGAACCGGACGTGGCCGTGTTGACGTCCAT  
GCTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGCGGAAGGTTGGCGAGGGGATC-6900  
ACCCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAAC  
TTGCAACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAG  
GCAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGA  
CTCCTTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCGAGAAAT  
CCTGCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGGGCGGACTATAA-7200  
CCCCCGCTAGTGGAGACGTGGAAAAAGCCGACTACGAACCACTGTGGTCCATGGTG  
TCCGCTTCCACCTCCAAAGTCCCCCTCTGTGCTCCGCTCGGAAGAAGCGGACGGTGGT  
CCTCACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAAGAAGCTTTGGCAG  
CTCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCCGCCCTTC  
TGGCTGCCCGCCGACTCCGACGCTGAGTCTATTCTCCTCATGCCCGCCCTGGAGGGGGA-7500  
GCCTGGGGATCCGGATCTTAGCGACGGGTATGGTCAACGGTCAGTAGTGAGGCAACGC  
GGAGGATGTCTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTACCCCCGTG  
CGCCGCGGAAGAACAGAAACTGCCATCAATGCACTAAGCAACTCGTTGCTACGTACCA  
CAATTTGGTGTATTCCACCACCTCAGCAGTGCTTGCCAAAGGCAGAAAGTACATT  
TGACAGACTGCAAGTTCTGGACAGCCATTACAGGACGTACTCAAGGAGGTTAAAGCAGC-7800  
GGCGTCAAAAGTGAAGGCTAAGTTGCTATCCGTAGAGGAAGCTTGACGCTGACGCCCC  
ACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAA  
GGCCGTAAACCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAAT  
AGACACTACCATCATGGCTAAGAACGAGGTTTCTGCGTTACGCTGAGAAGGGGGGTG  
TAAGCCAGCTCGTCTCATCGTGTTCGCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGC-8100  
TTTGTACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCTACGGATTCCA  
ATACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCC  
AATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCG  
TACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCTGGCCATCAA  
GTCCCTCACCAGAGGGCTTTATGTTGGGGGCCCTTTACCAATTCAAGGGGGGAGAAGT-8400  
CGGCTATCGCAGGTGCCGCGCAGCGGCGTACTGACAACAGCTGTGGTAAACCCCTCAC  
TTGCTACATCAAGGCCCGGGCAGCCTGTGAGCCGACGGGCTCCAGGACTGCACCATGCT  
CGTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGC  
GAGCCTGAGAGCCTTACGGAGGCTATGACCAGTACTCCGCCCCCTGGGGACCCCC  
ACAACCAGAAATACGACTTGGAGCTCATAACATCATGCTCCTCAAACGTGTCACTCGCCCA-8700  
CGACGGCGCTGGAAAGAGGGTCTACTACCTACCCGTGACCCTACAACCCCTCGCGAG  
AGCTGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCAT  
GTTTGGCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCTTAT  
AGCCAGGGACAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCAT  
AGAACCCTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACT-9000  
CCACAGTTACTCTCCAGGTGAAATTAATAGGGTGCCCGCATGCCTCAGAAAACCTTGGGGT

6  
ACCGCCCTTGGAGCTTGGAGACACCGGGCCGGAGCGTCCGCGCTAGGCTTCTGGCCAG  
AGGAGGCAGGGCTGCCATATGTGGCAAGTACCTCTCAACTGGGCAGTAAGAACAAAGCT  
CAAATCACTCAATAGCGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTACGCGCTGG  
CTACAGCGGGGAGACATTTATCACAGCGTGTCTCATGCCGGCCCCGCTGGATCTGGTT-9300  
TTGCTACTCTGCTTGTGCAAGGGGTAGGCATCTACCTCCTCCCAACCGATGAAGGTT  
GGGGTAAACACTCCGGCT-----3' terminus

Some clonal heterogeneities producing amino acid substitutions are shown. There are many other "silent mutations (not shown).



## FIG. 90A

R T  
MSTNPKPQKKNKRNTRRRQDVKFPGGGQIVGGVYLLPRRGPRLGVRATR  
KTSERSQPRGRRQPIPKARRPEGRWAQPGYPWPLYGNEGCGWAGWLLSP-100  
RGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARA

T  
LAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGL-200  
YHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNASRCWVAMTPTVATRD  
GKLPATQLRRHIDLLVGSATLCSALYVVDLCGSVFLVGQLFTFSPRRHWT-300

V  
TQGCNCSIYPGHITGHRMAWDMMNWSPTTALVMAQLLRIPQAILDMIAG  
AHWGLAGIAYFSMVGWAKVLVLLFAGVDAETHVTGGSAGHTVSGFV-400  
SLLAPGAKQNVQLINTNGSWHLNSTALNCNDSLNTGWLAGLFYHHKFNS  
GCPERLASCRPLTDFDQGWGPISYANGSGPDQRPYCWHYPPKPCGIVPAK-500  
SVCGPVYCFTSPVVGTTDRSGAPTYSWGENDTDFVLNNTRPPLGNWF  
GCTWMNSTGFTKVCGAPPCVIGGAGNNTLHCPTDCFRKHPDATYSRCGSG-600

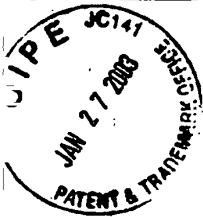
I  
PWLTPRCLVDYPYRLWHYPCTINYTIFKIRMYVGGVEHRLEAACNWTRGE  
RCDLEDNRSELSPLLLTTTQWQVLPSCFTTLPALSTGLIHLHQINVDVQ-700  
YLYGVGSSIASWAIKWEYVLLFLLADARVCSCWMLLISQAEAALEN  
LVILNAASLAGTHGLVSFLVFFCFAWYLGKGVPGAVYTFYGMWPLLLL-800

(N)  
LALPQRAYALDTEVAASC GGVLVGLMALTSPYYKRYISWCLWWLQYFL  
TRVEAQLHVWIPPLNVRGGRDAVILLMCAVHPTLVFDITKLLAVFGPLW-900  
ILQASLLKVYPYFVRVQGLLRFCALARKMIGGHYVQMVIIKLGALTGTYY  
NHLTPLRDWAHNGRLDLAVAVEPVVFSQMETKLITWGADTAACGDIINGL-1000  
PVSARRGREILLGPADGMVSKGWRLAPITAYAQQTRGLLGCITSLTGR  
DKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQM-1100

S T  
YTNDVQDLVGWPA PQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRG  
SLLSPRPISYLGSSGGP LCPAGHAVGIFRAAVCTRGVAKAVDFIPVEN-1200  
LETTMRSPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYK

L  
VLVLNPSVAATLGF GAYMSKAHGIDPNIRTVRTITTGSPITYSTYGKFL-1300  
ADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLTAT  
PPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRHILFCHSKKCC-1400  
DELA AKLVALGINAVAYYRGLDVS VIPTSGDVVVVATDALMTGYTGDFDS

Y (S)  
VIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSRTQRRGRTGRGKPGIYR-1500  
FVAPGERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPV  
CQDHLEFWEGVFTGLTHIDAHFLSQTQSGENLPYL VAYQATVCARAQAP-1600  
PPSWDQMWKCLIRLKPTLHGPTLLYRLGAVQNEITLTHPVTKYIMTCMS  
ADLEVVTSTWVLVGGVLAALAYCLSTGCVVIVGRVVL SGKPAIIPDREV-1700  
LYREFDEMEEC SQHLPYIEQGMMLAEQFKQKALGLLQTASRQAEVIAPAV  
QTNWQKLETFWAKHMMNFISGIQYLAGLSTLPGNPAIASLMAFTA AVTSP-1800  
LTSQTLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLID



## FIG. 90B

(G)  
ILAGYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVVCAA-1900

(HC)  
ILRRHVGPGEAVQWMNRLIAFASRGNHVSPTHYVPESDAAARVTAISSL  
LTVTQLLRRLHQWISSECTTPCSGSWLRDIWDWICEVLSDFKTWLKAKLM-2000

(V)  
PQLPGIPFVSCQRGYKGVWRGDGIMHTRCHCGAEITGHVKNGTMRIVGPR  
TCRNMWSGTFPINAYTTGCTPLPAPNYTFALWRVSAEEYVEIRQVGDH-2100  
YVTGMTDNLKCPQVPSPEFFTELDGVRHLRFAPPCKPLLREEVSFRVG  
LHEYVGSQLPCEPEPDVAVLTSMLTDPSHITAEAAAGRLARGSPPSVAS-2200  
SSASQLSAPSLKATCTANHDSFDAELIEANLLWRQEMGGNITRVESENKV  
VILDSFDPLVAEEDEREISVPAEILKSRRAQALPVWARPDPNPPLVET-2300

(S)  
WKKPDYEPVHVHGCPLPPKSPVPPPRKKRTVVLTSTALAEATR

(FA)  
SFGSSSTSGITGDNTTSSSEPAPSGCPPDSDAESYSSMPLEGEPPDL-2400  
SDGSWSTVSSEANAEDVCCSMSYSWTGALVTPCAEEQKLPINALSNL  
LRHNLVYSTTSRSACQRQKKVTFDRLQVLDVSHYQDVLKEVKAASKVKA-2500

(F)  
NLLSVEEACSLTPPHSAKSKFGYGAQDVRCARKAVTHINSVWKDLEDN  
VTPIDTTIMAKNEVFCVQPEKGGKPARLIVFPDLGVRVCEKMAFYDVVT-2600  
KLPLAVMGSSYGQYSPGQRVFLVQAWKSKKTPMGFSYDTRCFDSTVTE

(G)  
SDIRTEEAITYCCDLDPQARVAIKSLTERLYVGGPLTNSRGENCYRRCR-2700  
ASGVLTTCGNTLTCTYIKARAACRAAGLQDCTMLVCGDDLVCESAGVQ  
EDAASLRAFTEAMTRYSAAPPDPPQPEYDLELITSCSSNVSVAHGAGKR-2800  
VYYLTRDPTTPLARAAWETARHTFVNSWLGNIIIMFAPTLWARMILMTHFF  
SVLIARDQLEQALDCEIYGACYSIEPLDLPPIIQRHLGLSAFSLHSYSPG-2900

G  
EINRVAACLRKLGVPPLRAWHRARSVRARLLARGGAAICGKYLFWAV

(P)  
RTKLKLTPIAAAGQLDLGWFAGYSGGDIYHSVSHARPRWIWFCLLLLA-3000  
AGVGIYLLPNRO-3011

Stop codon

( ) = Heterogeneity due possibly  
to 5' or 3' terminal cloning  
artefact.

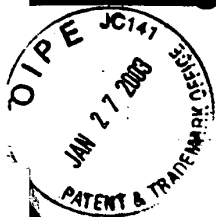


FIG. 91

